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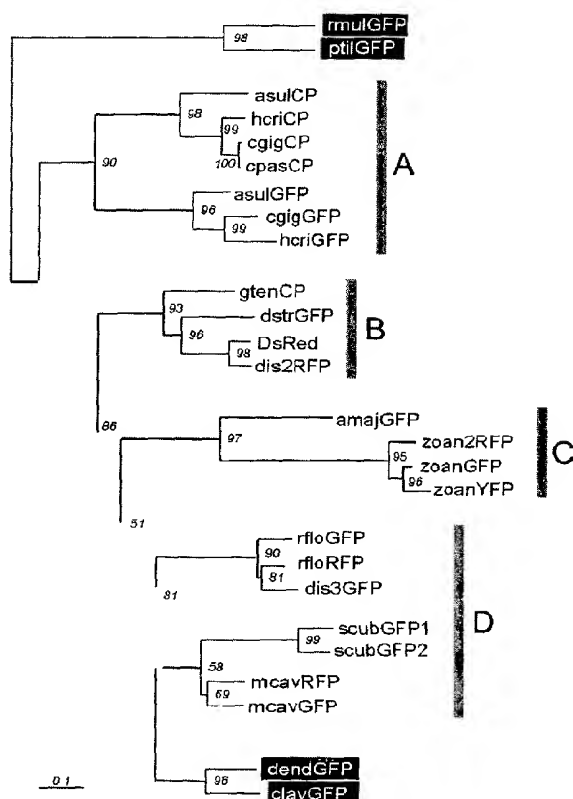
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- (71) Applicant (for all designated States except US): **CLON-TECH LABORATORIES, INC.** [US/US]; 1020 East Meadow Circle, Palo Alto, CA 94303 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **LABAS, Yulii,**

Aleksandrovich [RU/RU]; ul. Generala Tyuleneva d.35 kv. 416, 117465 Moscow (RU). **GURSKAYA, Nadezda, Georgievna** [RU/RU]; ul. Tsurupa d.7 kv.21, 113570 Moscow (RU). **YANUSHEVICH, Yuriy** [RU/RU]; ul. Bolshaya Cherkizovskaya, d. 3 korp 2. kv. 2, 107061 Moscow (RU). **FRADKOV, Arcady, Fedorovich** [RU/RU]; ul. Dnepropetrovskaya d. 35/2 kv. 14, 113570 Moscow (RU). **LUKYANOV, Konstantin** [RU/RU]; ul. Yuznobutovskay d. 60 kv. 21, 113570 Moscow (RU). **LUKYANOV, Sergey** [RU/RU]; ul. Yuznobutovskaya, d. 91 kv. 21, 113042 Moscow (RU). **MATZ, Mikhail, Vladimirovich** [US/RU]; ul. Teplyi stan d.7/2 kv.28, 117465 Moscow (RU).

(74) Agent: **FIELD, Bret, E.**; Bozicevic, Field & Francis, L.L.P., 200 Middlefield Road, Suite 200, Menlo Park, CA 94025 (US).

[Continued on next page]

(54) Title: NOVEL CHROMOPHORES/FLUOROPHORES AND METHODS FOR USING THE SAME



(57) Abstract: Nucleic acid compositions encoding novel chromo/fluoroproteins and mutants thereof, as well as the proteins encoded the same, are provided. The proteins of interest are proteins that are colored and/or fluorescent, where this feature arises from the interaction of two or more residues of the protein. The subject proteins are further characterized in that they are either obtained from non-bioluminescent Cnidarian, e.g., Anthozoan, species or are obtained from Anthozoan non-Pennatulacean (sea pen) species. Specific proteins of interest include the following specific proteins: hcriGFP; dendGFP; zoanRFP; scubGFP1; scubGFP2; rfloRFP; rfloGFP; mcavRFP; mcavGFP; cgigGFP; afraGFP; rfloGFP2; mcavGFP2; and mannFP. Also of interest are proteins that are substantially similar to, or mutants of, the above specific proteins. Also provided are fragments of the nucleic acids and the peptides encoded thereby, as well as antibodies to the subject proteins and transgenic cells and organisms. The subject protein and nucleic acid compositions find use in a variety of different applications. Finally, kits for use in such applications, e.g., that include the subject nucleic acid compositions, are provided.



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**NOVEL CHROMOPHORES/FLUOROPHORES AND
METHODS FOR USING THE SAME**
CROSS-REFERENCE TO RELATED APPLICATIONS

Pursuant to 35 U.S.C. § 119 (e), this application claims priority to the filing
5 date of United States Provisional Patent Application Serial No. 60/332,980 filed
November 13, 2001; the disclosure of which is herein incorporated by reference.

INTRODUCTION

Field of the Invention

10 The field of this invention is chromoproteins and fluorescent proteins.

Background of the Invention

Labeling is a tool for marking a protein, cell, or organism of interest and
plays a prominent role in many biochemistry, molecular biology and medical
diagnostic applications. A variety of different labels have been developed,
15 including radiolabels, chromolabels, fluorescent labels, chemiluminescent labels,
etc. However, there is continued interest in the development of new labels. Of
particular interest is the development of new protein labels, including chromo-
and/or fluorescent protein labels.

Relevant Literature

20 U.S. Patents of interest include: 6,066,476; 6,020,192; 5,985,577;
5,976,796; 5,968,750; 5,968,738; 5,958,713; 5,919,445; 5,874,304; and
5,491,084. International Patent Publications of interest include: WO 00/46233;
WO 99/49019; and DE 197 18 640 A. Also of interest are: Anderluh et al.,
Biochemical and Biophysical Research Communications (1996) 220:437-442;
25 Dove et al., Biological Bulletin (1995) 189:288-297; Fradkov et al., FEBS Lett.
(2000) 479(3):127-30; Gurskaya et al., FEBS Lett., (2001) 507(1):16-20; Gurskaya
et al., BMC Biochem. (2001) 2:6; Lukyanov, K., et al (2000) J Biol Chemistry
275(34):25879-25882; Macek et al., Eur. J. Biochem. (1995) 234:329-335;
Martynov et al., J Biol Chem. (2001) 276:21012-6; Matz, M.V., et al. (1999) Nature
30 Biotechnol., 17:969-973; Tersikh et al., Science (2000) 290:1585-8; Tsien, Annual
Rev. of Biochemistry (1998) 67:509-544; Tsien, Nat. Biotech. (1999) 17:956-957;
Ward et al., J. Biol. Chem. (1979) 254:781-788; Wiedermann et al., Jahrestagung

der Deutschen Gesellschaft für Tropenökologie-gto. Ulm. 17-19.02.1999. Poster P-4.20; Yarbrough et al., Proc Natl Acad Sci U S A (2001) 98:462-7.

SUMMARY OF THE INVENTION

5 Nucleic acid compositions encoding novel chromo/fluoroproteins and mutants thereof, as well as the proteins encoded the same, are provided. The proteins of interest are proteins that are colored and/or fluorescent, where this feature arises from the interaction of two or more residues of the protein. The subject proteins are further characterized in that they are either obtained from non-

10 bioluminescent Cnidarian, e.g., Anthozoan, species or are obtained from Anthozoan non-Pennatulacean (sea pen) species. Specific proteins of interest include the following specific proteins: (1) Green fluorescent protein from *Heteractis crispa* (hcriGFP); (2) Green fluorescent protein from *Dendronephthya* sp. (dendGFP); (3) Red fluorescent protein from *Zoanthus* sp. (zoanRFP); (4)

15 Green fluorescent protein from *Scolymia cubensis* (scubGFP1); (5) Green fluorescent protein from *Scolymia cubensis* (scubGFP2); (6) Red fluorescent protein from *Ricordea florida* (rfloRFP); (7) Green fluorescent protein from *Ricordea florida* (rfloGFP); (8) Red fluorescent protein from *Montastraea cavernosa* (mcavRFP); (9) Green fluorescent protein from *Montastraea cavernosa*

20 (mcavGFP); (10) Green fluorescent protein from *Condylactis gigantea* (cgigGFP); (11) Green fluorescent protein from *Agaricia fragilis* (afraGFP); (12) Green fluorescent protein from *Ricordea florida* (rfloGFP2); (13) Green fluorescent protein from *Montastraea cavernosa* (mcavGFP2); and (14) Green fluorescent protein homolog from *Montastraea annularis* (mannFP). Also of interest are

25 proteins that are substantially similar to, or mutants of, the above specific proteins. Also provided are fragments of the nucleic acids and the peptides encoded thereby, as well as antibodies to the subject proteins and transgenic cells and organisms. The subject protein and nucleic acid compositions find use in a variety of different applications. Finally, kits for use in such applications, e.g., that include

30 the subject nucleic acid compositions, are provided.

BREIF DESCRIPTION OF THE FIGURES

Figure 1. Changes of emission spectra during maturation of the new red-emitters: zoan2RFP (A, B), mcavRFP (C, D) and rfloRFP (E, F). The excitation

wavelength is given within each graph. Horizontal axis is wavelength in nanometers, vertical axis is fluorescence intensity. Maturation stages: A, C, E – early; B, D, F – late (see Methods for details). All the three proteins exhibit “timer” phenotype (green emission at first and red emission arising later). Note that

5 zoan2RFP matures significantly faster than mcavRFP and rfloRFP: even at the “early” stage the red emission peak is very pronounced, and by the “late” stage the protein converts into red completely. In contrast, mcavRFP and rfloRFP fail to undergo such a complete maturation.

Figure 2. Details on excitation spectra of mcavRFP (A, B) and rfloRFP (C, D). Wavelengths at which the emission was monitored are given within the graphs. A, C: excitation spectra of the green emission band in the immature protein, lacking the red emission; B, D: excitation spectra of the red emission band in more mature form. Horizontal axis is wavelength in nanometers, vertical axis is fluorescence intensity. Note that in both proteins, the major excitation peaks for

10

15 immature green and mature red forms are virtually identical to each other.

Figure 3. The maximum-likelihood phylogenetic tree for the current dataset of anthozoan GFP-like proteins. Numbers at nodes denote the quartet-puzzling support values (1000 puzzling attempts). Proteins from Alcyonaria sub-class, which were considered outgroups, are labeled in white on black. The “stem” of the tree (thick gray line), joining two rooting groups, putatively reflects the diversity of GFP-like proteins before the separation of Alcyonaria and Zoantharia sub-classes. Gray bars marked A, B, C and D denote four distinct clades of GFP-like proteins found in Zoantharia. Scale bar: 0.1 replacements/site.

20

Figure 4. Summary of spectral features and chromophore structures in the family of GFP-like proteins. Note that this paper uses different names for GFP-like proteins than proposed in original publications (the original names, where available, are given in brackets in the first column; see text for nomenclature details).

25

Figure 5. Summary of the major clades of GFP-like proteins from sub-class Zoantharia.

30

Figure 6. Excitation (solid lines) and emission (dotted lines) spectra for the GFP-like proteins reported in this paper. The wavelengths at which the excitation or emission curves were taken are given in the legend to each graph. Horizontal

axis is wavelength in nanometers, vertical axis is fluorescence intensity. The graphs for the two new orange-red proteins are boxed.

Figure 7. Alignment of the currently cloned and spectroscopically characterized GFP-like proteins. Numeration above the alignment is according to GFP from *Aequorea victoria*.

Figure 8 provides the nucleotide and amino acid sequence of wild type *Heteractis crispa* hcriGFP. (SEQ ID NO:01 & 02)

Figure 9 provides the nucleotide and amino acid sequence of wild type *Dendronephthya* sp. dendGFP. (SEQ ID NO:03 & 04)

10 Figure 10 provides the nucleotide and amino acid sequence of wild type *Zoanthus* sp. zoanRFP. (SEQ ID NO:05 & 06)

Figure 11 provides the nucleotide and amino acid sequence of wild type *Scolymia cubensis* scubGFP1. (SEQ ID NO:07 & 08)

15 Figure 12 provides the nucleotide and amino acid sequence of wild type *Scolymia cubensis* scubGFP2. (SEQ ID NO:09 & 10)

Figure 13 provides the nucleotide and amino acid sequence of wild type *Ricordea florida* rfloRFP. (SEQ ID NO:11 & 12)

Figure 14 provides the nucleotide and amino acid sequence of wild type *Ricordea florida* rfloGFP. (SEQ ID NO:13 & 14)

20 Figure 15 provides the nucleotide and amino acid sequence of wild type *Montastraea cavernosa* mcavRFP. (SEQ ID NO:15 & 16)

Figure 16 provides the nucleotide and amino acid sequence of wild type *Montastraea cavernosa* mcavGFP. (SEQ ID NO:17 & 18)

25 Figure 17 provides the nucleotide and amino acid sequence of wild type *Condylactis gigantea* cgigGFP. (SEQ ID NO: 19 & 20).

Figure 18 provides the nucleotide and amino acid sequence of wild type *Agaricia fragilis* afraGFP. (SEQ ID NO: 21& 22).

Figure 19 provides the nucleotide and amino acid sequence of wild type *Ricordea florida* rfloGFP2. (SEQ ID NO: 23& 24).

30 Figure 20 provides the nucleotide and amino acid sequence of wild type *Montastraea cavernosa* mcavGFP2. (SEQ ID NO: 25& 26).

Figure 21 provides the nucleotide and amino acid sequence of wild type *Montastraea annularis* mannFP. (SEQ ID NO: 27& 28).

FEATURES OF THE INVENTION

The subject invention provides a nucleic acid present in other than its natural environment, wherein the nucleic acid encodes a chromo- or fluorescent protein and is from a non-bioluminescent Cnidarian species. In certain embodiments, the non-bioluminescent Cnidarian species is an Anthozoan species. In certain embodiments, the nucleic acid is isolated. In certain embodiments, the nucleic acid is present in other than its natural environment, where the nucleic acid encodes an Anthozoan chromo- or fluorescent protein and is from a non-Pennatulacean Anthozoan species. In certain embodiments, the nucleic acid has a sequence of residues that is substantially the same as or identical to a nucleotide sequence of at least 10 residues in length of SEQ ID NOS:01, 03, 05, 07, 09, 11, 13, 15, 17; 19; 21; 23; 25; and 27. In certain embodiments, the nucleic acid has a sequence similarity of at least about 60% with a sequence of at least 10 residues in length selected from the group of sequences consisting of SEQ ID NOS:01, 03, 05, 07, 09, 11, 13, 15, 17; 19; 21; 23; 25; and 27. In certain embodiments, the nucleic acid encodes a chromo and/or fluorescent protein that is either: (a) from a non-bioluminescent Cnidarian species; or (b) from a non-Pennatulacean Anthozoan species. In certain embodiments, the nucleic acid encodes a protein that has an amino acid sequence selected from the group consisting of: SEQ ID NOS: 02; 04; 06; 08; 10; 12; 14; 16; 18; 20; 22; 24; 26; and 28. In certain embodiments, the nucleic acid encodes a mutant protein of a chromo and/or fluorescent protein that is either: (a) from a non-bioluminescent Cnidarian species; or (b) from a non-Pennatulacean Anthozoan species; where in certain embodiments the mutant protein comprises at least one point mutation as compared to its wild type protein; and in other embodiments the mutant protein comprises at least one deletion mutation as compared to its wild type protein.

Also provided are fragments of the provided nucleic acids. Also provided are isolated nucleic acids or mimetics thereof that hybridize under stringent conditions to the provided nucleic acids. Also provided are constructs comprising a vector and a nucleic acid of the present invention. Also provided are expression cassettes that include: (a) a transcriptional initiation region functional in an expression host; (b) a nucleic acid of the present invention; and (c) a transcriptional termination region functional in said expression host. Also provided

are cells, or the progeny thereof, comprising an expression cassette of the present invention as part of an extrachromosomal element or integrated into the genome of a host cell as a result of introduction of said expression cassette into said host cell.

5 Also provided are methods of producing a chromo and/or fluorescent protein that include: growing a cell of the present invention, whereby said protein is expressed; and isolating said protein substantially free of other proteins.

Also provided are proteins or fragments thereof encoded by a nucleic acid of the present invention.

10 Also provided are antibodies binding specifically to a protein of the present invention.

Also provided are transgenic cells or the progeny thereof that include a transgene selected that includes a nucleic acid of the present invention.

Also provided are transgenic organisms that include a transgene that
15 includes a nucleic acid of the present invention.

Also provided are applications that employ a chromo- or fluorescent protein
of the present invention.

Also provided are applications that employ a nucleic acid encoding a
chromo- or fluorescent protein of the present invention.

20 Also provided are kits that include a nucleic acid according the subject invention and instructions for using said nucleic acid.

DEFINITIONS

In accordance with the present invention there may be employed
25 conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D.N. Glover ed. 1985); "Oligonucleotide Synthesis" (M.J. Gait ed. 1984); "Nucleic Acid
30 Hybridization" (B.D. Hames & S.J. Higgins eds. (1985)); "Transcription and Translation" (B.D. Hames & S.J. Higgins eds. (1984)); "Animal Cell Culture" (R.I. Freshney, ed. (1986)); "Immobilized Cells and Enzymes" (IRL Press, (1986)); B. Perbal, "A Practical Guide To Molecular Cloning" (1984).

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in either single stranded form or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, inter alia, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes.

A DNA "coding sequence" is a DNA sequence which is transcribed and translated into a polypeptide in vivo when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g., mammalian) DNA, and synthetic DNA sequences. A polyadenylation signal and transcription termination sequence may be located 3' to the coding sequence.

As used herein, the term "hybridization" refers to the process of association of two nucleic acid strands to form an antiparallel duplex stabilized by means of hydrogen bonding between residues of the opposite nucleic acid strands.

The term "oligonucleotide" refers to a short (under 100 bases in length) nucleic acid molecule.

"DNA regulatory sequences", as used herein, are transcriptional and translational control sequences, such as promoters, enhancers, polyadenylation signals, terminators, and the like, that provide for and/or regulate expression of a coding sequence in a host cell.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site, as well as

protein binding domains responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Various promoters, including inducible promoters, may be used to drive the various vectors of the present invention.

5 As used herein, the terms "restriction endonucleases" and "restriction enzymes" refer to bacterial enzymes, each of which cut double-stranded DNA at or near a specific nucleotide sequence.

 A cell has been "transformed" or "transfected" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. The
10 transforming DNA may or may not be integrated (covalently linked) into the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the transforming DNA may be maintained on an episomal element such as a plasmid. With respect to eukaryotic cells, a stably transformed cell is one in which the transforming DNA has become integrated into a chromosome so that it is inherited
15 by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the transforming DNA. A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for
20 many generations.

 A "heterologous" region of the DNA construct is an identifiable segment of DNA within a larger DNA molecule that is not found in association with the larger molecule in nature. Thus, when the heterologous region encodes a mammalian gene, the gene will usually be flanked by DNA that does not flank the mammalian
25 genomic DNA in the genome of the source organism. In another example, heterologous DNA includes coding sequence in a construct where portions of genes from two different sources have been brought together so as to produce a fusion protein product. Allelic variations or naturally-occurring mutational events do not give rise to a heterologous region of DNA as defined herein.

30 As used herein, the term "reporter gene" refers to a coding sequence attached to heterologous promoter or enhancer elements and whose product may be assayed easily and quantifiably when the construct is introduced into tissues or cells.

The amino acids described herein are preferred to be in the "L" isomeric form. The amino acid sequences are given in one-letter code (A: alanine; C: cysteine; D: aspartic acid; E: glutamic acid; F: phenylalanine; G: glycine; H: histidine; I: isoleucine; K: lysine; L: leucine; M: methionine; N: asparagine; P: proline; Q: glutamine; R: arginine; S: serine; T: threonine; V: valine; W: tryptophan; Y: tyrosine; X: any residue). NH₂ refers to the free amino group present at the amino terminus of a polypeptide. COOH refers to the free carboxy group present at the carboxy terminus of a polypeptide. In keeping with standard polypeptide nomenclature, *J Biol. Chem.*, 243 (1969), 3552-59 is used.

The term "immunologically active" defines the capability of the natural, recombinant or synthetic chromo/fluorescent protein, or any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies. As used herein, "antigenic amino acid sequence" means an amino acid sequence that, either alone or in association with a carrier molecule, can elicit an antibody response in a mammal. The term "specific binding," in the context of antibody binding to an antigen, is a term well understood in the art and refers to binding of an antibody to the antigen to which the antibody was raised, but not other, unrelated antigens.

As used herein the term "isolated" is meant to describe a polynucleotide, a polypeptide, an antibody, or a host cell that is in an environment different from that in which the polynucleotide, the polypeptide, the antibody, or the host cell naturally occurs.

Bioluminescence (BL) is defined as emission of light by living organisms that is well visible in the dark and affects visual behavior of animals (See e.g., Harvey, E. N. (1952). *Bioluminescence*. New York: Academic Press; Hastings, J. W. (1995). *Bioluminescence*. In: *Cell Physiology* (ed. by N. Speralakis). pp. 651-681. New York: Academic Press.; Wilson, T. and Hastings, J. W. (1998). *Bioluminescence. Annu Rev Cell Dev Biol* **14**, 197-230.). Bioluminescence does not include so-called ultra-weak light emission, which can be detected in virtually all living structures using sensitive luminometric equipment (Murphy, M. E. and Sies, H.(1990). Visible-range low-level chemiluminescence in biological systems. *Meth.Enzymol.***186**, 595-610; Radotic, K, Radenovic, C, Jeremic, M. (1998.) Spontaneous ultra-weak bioluminescence in plants: origin, mechanisms and

properties. *Gen Physiol Biophys* **17**, 289-308), and from weak light emission which most probably does not play any ecological role, such as the glowing of bamboo growth cone (Totsune, H., Nakano, M., Inaba, H.(1993). Chemiluminescence from bamboo shoot cut. *Biochem. Biophys. Res Comm.* **194**, 1025-1029) or emission of light during fertilization of animal eggs (Klebanoff, S. J., Froeder, C. A., Eddy, E. M., Shapiro, B. M. (1979). Metabolic similarities between fertilization and phagocytosis. Conservation of peroxidatic mechanism. *J. Exp. Med.* **149**, 938-953; Schomer, B. and Epel, D. (1998). Redox changes during fertilization and maturation of marine invertebrate eggs. *Dev Biol* **203**, 1-11).

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Nucleic acid compositions encoding novel chromo/fluoroproteins and mutants thereof, as well as the proteins encoded the same, are provided. The proteins of interest are proteins that are colored and/or fluorescent, where this feature arises from the interaction of two or more residues of the protein. The subject proteins are further characterized in that they are either obtained from non-bioluminescent Cnidarian, e.g., Anthozoan; species or are obtained from non-Pennatulacean (sea pen) Anthozoan species. Specific proteins of interest include the following specific proteins: (1) Green fluorescent protein from *Heteractis crispa* (hcriGFP); (2) Green fluorescent protein from *Dendronephthya* sp. (dendGFP); (3) Red fluorescent protein from *Zoanthus* sp. (zoanRFP); (4) Green fluorescent protein from *Scolymia cubensis* (scubGFP1); (5) Green fluorescent protein from *Scolymia cubensis* (scubGFP2); (6) Red fluorescent protein from *Ricordea florida* (rfloRFP); (7) Green fluorescent protein from *Ricordea florida* (rfloGFP); (8) Red fluorescent protein from *Montastraea cavernosa* (mcavRFP); (9) Green fluorescent protein from *Montastraea cavernosa* (mcavGFP); (10) Green fluorescent protein from *Condylactis gigantea* (cgigGFP); (11) Green fluorescent protein from *Agaricia fragilis* (afraGFP); (12) Green fluorescent protein from *Ricordea florida* (rfloGFP2); (13) Green fluorescent protein from *Montastraea cavernosa* (mcavGFP2); and (14) Green fluorescent protein homolog from *Montastraea annularis* (mannFP). Also of interest are proteins that are substantially similar to, or mutants of, the above specific proteins. Also provided are fragments of the nucleic acids and the peptides encoded thereby, as well as antibodies to the subject proteins, and

transgenic cells and organisms that include the subject nucleic acid/protein compositions. The subject protein and nucleic acid compositions find use in a variety of different applications. Finally, kits for use in such applications, e.g., that include the subject nucleic acid compositions, are provided.

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Before the subject invention is described further, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

In this specification and the appended claims, the singular forms "a," "an" and "the" include plural reference unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range, and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices and materials similar or equivalent to those described herein can be used in the practice or

testing of the invention, the preferred methods, devices and materials are now described.

5 All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the cell lines, vectors, methodologies and other invention components that are described in the publications which might be used in connection with the presently described invention.

10 In further describing the subject invention, the subject nucleic acid compositions will be described first, followed by a discussion of the subject protein compositions, antibody compositions and transgenic cells/organisms. Next a review of representative methods in which the subject proteins find use is provided.

15 NUCLEIC ACID COMPOSITIONS

As summarized above, the subject invention provides nucleic acid compositions encoding chromo- and fluoroproteins and mutants thereof, as well as fragments and homologues of these proteins. By chromo and/or fluorescent protein is meant a protein that is colored, i.e., is pigmented, where the protein may or may not be fluorescent, e.g., it may exhibit low, medium or high fluorescence upon irradiation with light of an excitation wavelength. In any event, the subject proteins of interest are those in which the colored characteristic, i.e., the chromo and/or fluorescent characteristic, is one that arises from the interaction of two or more residues of the protein, and not from a single residue, more specifically a single side chain of a single residue, of the protein. As such, fluorescent proteins of the subject invention do not include proteins that exhibit fluorescence only from residues that act by themselves as intrinsic fluors, i.e., tryptophan, tyrosine and phenylalanine. As such, the fluorescent proteins of the subject invention are fluorescent proteins whose fluorescence arises from some structure in the protein that is other than the above specified single residues, e.g., it arises from an interaction of two or more residues.

By nucleic acid composition is meant a composition comprising a sequence of DNA having an open reading frame that encodes a chromo/fluoro polypeptide of

the subject invention, i.e., a chromo/fluoroprotein gene, and is capable, under appropriate conditions, of being expressed as a chromo/fluoro protein according to the subject invention. Also encompassed in this term are nucleic acids that are homologous, substantially similar or identical to the nucleic acids of the present invention. Thus, the subject invention provides genes and coding sequences thereof encoding the proteins of the subject invention, as well as homologs thereof. The subject nucleic acids are present in other than their natural environment, e.g., they are isolated, present in enriched amounts, etc., from their naturally occurring environment, e.g., the organism from which they are obtained.

The nucleic acids are further characterized in that they encode proteins that are either from: (1) non-bioluminescent species, often non-bioluminescent Cnidarian species, e.g., non-bioluminescent Anthozoan species; or (2) from Anthozoan species that are not Pennatulacean species, i.e., that are not sea pens. As such, the nucleic acids may encode proteins from bioluminescent Anthozoan species, so long as these species are not Pennatulacean species, e.g., that are not Renillan or Ptilosarcian species. Specific nucleic acids of interest are those that encode the following specific proteins: (1) Green fluorescent protein from *Heteractis crispa* (hcriGFP) (Genbank Accession No. AF420592); (2) Green fluorescent protein from *Dendronephthya* sp. (dendGFP) (Genbank Accession No. AF420591); (3) Red fluorescent protein from *Zoanthus* sp. (zoanRFP) (Genbank Accession No. AY059642); (4) Green fluorescent protein from *Scolymia cubensis* (scubGFP1) (Genbank Accession No. AY037767); (5) Green fluorescent protein from *Scolymia cubensis* (scubGFP2) (Genbank Accession No. AY037771); (6) Red fluorescent protein from *Ricordea florida* (rfloRFP) (Genbank Accession No. AY037773); (7) Green fluorescent protein from *Ricordea florida* (rfloGFP) (Genbank Accession No. AY037772); (8) Red fluorescent protein from *Montastraea cavernosa* (mcavRFP) (Genbank Accession No. AY037770); (9) Green fluorescent protein from *Montastraea cavernosa* (mcavGFP) (Genbank Accession No. AY037769); (10) Green fluorescent protein from *Condylactis gigantea* (cgigGFP) (Genbank Accession No. AY03776); (11) Green fluorescent protein from *Agaricia fragilis* (afraGFP); (12) Green fluorescent protein from *Ricordea florida* (rfloGFP2); (13) Green fluorescent protein from *Montastraea cavernosa* (mcavGFP2); and (14) Green fluorescent protein homolog from

Montastraea annularis (mannFP). Also of interest are derived from, or are mutants, homologues of, the above specific nucleic acids.

In addition to the above described specific nucleic acid compositions, also of interest are homologues of the above sequences. With respect to homologues of the subject nucleic acids, the source of homologous genes may be any species of plant or animal or the sequence may be wholly or partially synthetic. In certain embodiments, sequence similarity between homologues is at least about 20%, sometimes at least about 25 %, and may be 30 %, 35%, 40%, 50%, 60%, 70% or higher, including 75%, 80%, 85%, 90% and 95% or higher. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul *et al.* (1990), *J. Mol. Biol.* 215:403-10 (using default settings, i.e. parameters $w=4$ and $T=17$). The sequences provided herein are essential for recognizing related and homologous nucleic acids in database searches. Of particular interest in certain embodiments are nucleic acids of substantially the same length as the nucleic acid identified as SEQ ID NOS: 01, 03, 05, 07, 09, 11, 13, 15, 17, 19, 21, 23, 25 or 27, where by substantially the same length is meant that any difference in length does not exceed about 20 number %, usually does not exceed about 10 number % and more usually does not exceed about 5 number %; and have sequence identity to any of these sequences of at least about 90%, usually at least about 95% and more usually at least about 99% over the entire length of the nucleic acid. In many embodiments, the nucleic acids have a sequence that is substantially similar (i.e. the same as) or identical to the sequences of SEQ ID NOS: 01, 03, 05, 07, 09, 11, 13, 15, 17, 21, 23, 25, 27. By substantially similar is meant that sequence identity will generally be at least about 60%, usually at least about 75% and often at least about 80, 85, 90, or even 95%.

Also provided are nucleic acids that encode the proteins encoded by the above described nucleic acids, but differ in sequence from the above described nucleic acids due to the degeneracy of the genetic code.

Also provided are nucleic acids that hybridize to the above described nucleic acid under stringent conditions. An example of stringent hybridization conditions is hybridization at 50°C or higher and 0.1×SSC (15 mM sodium chloride/1.5 mM sodium citrate). Another example of stringent hybridization conditions is overnight incubation at 42°C in a solution: 50 % formamide, 5 × SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5 × Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 × SSC at about 65°C. Stringent hybridization conditions are hybridization conditions that are at least as stringent as the above representative conditions, where conditions are considered to be at least as stringent if they are at least about 80% as stringent, typically at least about 90% as stringent as the above specific stringent conditions. Other stringent hybridization conditions are known in the art and may also be employed to identify nucleic acids of this particular embodiment of the invention.

Nucleic acids encoding mutants of the proteins of the invention are also provided. Mutant nucleic acids can be generated by random mutagenesis or targeted mutagenesis, using well-known techniques which are routine in the art. In some embodiments, chromo- or fluorescent proteins encoded by nucleic acids encoding homologues or mutants have the same fluorescent properties as the wild-type fluorescent protein. In other embodiments, homologue or mutant nucleic acids encode chromo- or fluorescent proteins with altered spectral properties, as described in more detail herein.

One category of mutant that is of particular interest is the non-aggregating mutant. In many embodiments, the non-aggregating mutant differs from the wild type sequence by a mutation in the N-terminus that modulates the charges appearing on side groups of the N-terminus residues, e.g., to reverse or neutralize the charge, in a manner sufficient to produce a non-aggregating mutant of the naturally occurring protein or mutant, where a particular protein is considered to be non-aggregating if it is determined to be non-aggregating using the assay reported in U.S. Patent Application serial no. 60/270,983, the disclosure of which is herein incorporated by reference.

Another category of mutant of particular interest is the modulated oligomerization mutant. A mutant is considered to be a modulated oligomerization

mutant if its oligomerization properties are different as compared to the wild type protein. For example, if a particular mutant oligomerizes to a greater or lesser extent than the wild type, it is considered to be an oligomerization mutant. Of particular interest are oligomerization mutants that do not oligomerize, i.e., are
5 monomers under physiological (e.g., intracellular) conditions, or oligomerize to a lesser extent than the wild type, e.g., are dimers or trimers under intracellular conditions.

Nucleic acids of the subject invention may be cDNA or genomic DNA or a fragment thereof. In certain embodiments, the nucleic acids of the subject
10 invention include one or more of the open reading frames encoding specific fluorescent proteins and polypeptides, and introns, as well as adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The subject nucleic acids may be introduced into an appropriate vector for
15 extrachromosomal maintenance or for integration into a host genome, as described in greater detail below.

The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA
species, where sequence elements are exons and 5' and 3' non-coding regions.
20 Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding the protein.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed
25 sequences, including all of the introns that are normally present in a native chromosome. It may further include 5' and 3' un-translated regions found in the mature mRNA. It may further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' or 3' end of the
30 transcribed region. The genomic DNA may be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' or 5', or internal regulatory

sequences as sometimes found in introns, contains sequences required for proper tissue and stage specific expression.

The nucleic acid compositions of the subject invention may encode all or a part of the subject proteins. Double or single stranded fragments may be obtained
5 from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* For the most part, DNA fragments will be of at least about 15 nt, usually at least about 18 nt or about 25 nt, and may be at least about 50 nt. In some embodiments, the subject nucleic acid molecules may be about 100 nt,
10 about 200 nt, about 300 nt, about 400 nt, about 500 nt, about 600 nt, about 700 nt, or about 720 nt in length. The subject nucleic acids may encode fragments of the subject proteins or the full-length proteins, e.g., the subject nucleic acids may encode polypeptides of about 25 aa, about 50 aa, about 75 aa, about 100 aa, about 125 aa, about 150 aa, about 200 aa, about 210 aa, about 220 aa, about 230
15 aa, or about 240 aa, up to the entire protein.

The subject nucleic acids are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the DNA will be obtained substantially free of other nucleic acid sequences that do not include a nucleic acid of the subject invention or fragment thereof, generally being at least about
20 50%, usually at least about 90% pure and are typically "recombinant", *i.e.* flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The subject polynucleotides (e.g., a polynucleotide having a sequence of SEQ ID NOS: 01, 03, 05, 07, 09, 11, 13, 15, 17, 19, 21, 23, 25, 27 etc.), the
25 corresponding cDNA, the full-length gene and constructs of the subject polynucleotides are provided. These molecules can be generated synthetically by a number of different protocols known to those of skill in the art. Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring
30 Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research.

Also provided are nucleic acids that encode fusion proteins of the subject proteins, or fragments thereof, which are fused to a second protein, e.g., a degradation sequence, a signal peptide, etc. Fusion proteins may comprise a subject polypeptide, or fragment thereof, and a non-Anthozoan polypeptide ("the fusion partner") fused in-frame at the N-terminus and/or C-terminus of the subject polypeptide. Fusion partners include, but are not limited to, polypeptides that can bind antibody specific to the fusion partner (e.g., epitope tags); antibodies or binding fragments thereof; polypeptides that provide a catalytic function or induce a cellular response; ligands or receptors or mimetics thereof; and the like. In such fusion proteins, the fusion partner is generally not naturally associated with the subject Anthozoan portion of the fusion protein, and is typically not an Anthozoan protein or derivative/fragment thereof, i.e., it is not found in Anthozoan species.

Also provided are constructs comprising the subject nucleic acids inserted into a vector, where such constructs may be used for a number of different applications, including propagation, protein production, etc. Viral and non-viral vectors may be prepared and used, including plasmids. The choice of vector will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. To prepare the constructs, the partial or full-length polynucleotide is inserted into a vector typically by means of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence can be inserted by homologous recombination in vivo. Typically this is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence. Regions of homology are added by ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion of the desired nucleotide sequence, for example.

Also provided are expression cassettes or systems that find use in, among other applications, the synthesis of the subject proteins. For expression, the gene product encoded by a polynucleotide of the invention is expressed in any convenient expression system, including, for example, bacterial, yeast, insect,

amphibian and mammalian systems. Suitable vectors and host cells are described in U.S. Patent No. 5,654,173. In the expression vector, a subject polynucleotide, e.g., as set forth in SEQ ID NOS:01; 03; 05; 07; 09; 11; 13; 15; 17; 19; 21; 23; 25 or 27, is linked to a regulatory sequence as appropriate to obtain the desired expression properties. These regulatory sequences can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used. In other words, the expression vector will provide a transcriptional and translational initiation region, which may be inducible or constitutive, where the coding region is operably linked under the transcriptional control of the transcriptional initiation region, and a transcriptional and translational termination region. These control regions may be native to the subject species from which the subject nucleic acid is obtained, or may be derived from exogenous sources.

Expression vectors generally have convenient restriction sites located near the promoter sequence to provide for the insertion of nucleic acid sequences encoding heterologous proteins. A selectable marker operative in the expression host may be present. Expression vectors may be used for, among other things, the production of fusion proteins, as described above.

Expression cassettes may be prepared comprising a transcription initiation region, the gene or fragment thereof, and a transcriptional termination region. Of particular interest is the use of sequences that allow for the expression of functional epitopes or domains, usually at least about 8 amino acids in length, more usually at least about 15 amino acids in length, to about 25 amino acids, and up to the complete open reading frame of the gene. After introduction of the DNA, the cells containing the construct may be selected by means of a selectable marker, the cells expanded and then used for expression.

The above described expression systems may be employed with prokaryotes or eukaryotes in accordance with conventional ways, depending upon the purpose for expression. For large scale production of the protein, a unicellular

organism, such as *E. coli*, *B. subtilis*, *S. cerevisiae*, insect cells in combination with baculovirus vectors, or cells of a higher organism such as vertebrates, e.g. COS 7 cells, HEK 293, CHO, *Xenopus* Oocytes, etc., may be used as the expression host cells. In some situations, it is desirable to express the gene in eukaryotic cells, where the expressed protein will benefit from native folding and post-translational modifications. Small peptides can also be synthesized in the laboratory. Polypeptides that are subsets of the complete protein sequence may be used to identify and investigate parts of the protein important for function.

Specific expression systems of interest include bacterial, yeast, insect cell and mammalian cell derived expression systems. Representative systems from each of these categories is are provided below:

Bacteria. Expression systems in bacteria include those described in Chang *et al.*, *Nature* (1978) 275:615; Goeddel *et al.*, *Nature* (1979) 281:544; Goeddel *et al.*, *Nucleic Acids Res.* (1980) 8:4057; EP 0 036,776; U.S. Patent No. 4,551,433; DeBoer *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:21-25; and Siebenlist *et al.*, *Cell* (1980) 20:269.

Yeast. Expression systems in yeast include those described in Hinnen *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1978) 75:1929; Ito *et al.*, *J. Bacteriol.* (1983) 153:163; Kurtz *et al.*, *Mol. Cell. Biol.* (1986) 6:142; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Gleeson *et al.*, *J. Gen. Microbiol.* (1986) 132:3459; Roggenkamp *et al.*, *Mol. Gen. Genet.* (1986) 202:302; Das *et al.*, *J. Bacteriol.* (1984) 158:1165; De Louvencourt *et al.*, *J. Bacteriol.* (1983) 154:737; Van den Berg *et al.*, *Bio/Technology* (1990) 8:135; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Cregg *et al.*, *Mol. Cell. Biol.* (1985) 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555; Beach and Nurse, *Nature* (1981) 300:706; Davidow *et al.*, *Curr. Genet.* (1985) 10:380; Gaillardin *et al.*, *Curr. Genet.* (1985) 10:49; Ballance *et al.*, *Biochem. Biophys. Res. Commun.* (1983) 112:284-289; Tilburn *et al.*, *Gene* (1983) 26:205-221; Yelton *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1984) 81:1470-1474; Kelly and Hynes, *EMBO J.* (1985) 4:475479; EP 0 244,234; and WO 91/00357.

Insect Cells. Expression of heterologous genes in insects is accomplished as described in U.S. Patent No. 4,745,051; Friesen *et al.*, "The Regulation of Baculovirus Gene Expression", in: *The Molecular Biology Of Baculoviruses* (1986) (W. Doerfler, ed.); EP 0 127,839; EP 0 155,476; and Vlak *et al.*, *J. Gen. Virol.*

(1988) 69:765-776; Miller *et al.*, *Ann. Rev. Microbiol.* (1988) 42:177; Carbonell *et al.*, *Gene* (1988) 73:409; Maeda *et al.*, *Nature* (1985) 315:592-594; Lebacqz-Verheyden *et al.*, *Mol. Cell. Biol.* (1988) 8:3129; Smith *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1985) 82:8844; Miyajima *et al.*, *Gene* (1987) 58:273; and Martin *et al.*, *DNA* (1988) 7:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts are described in Luckow *et al.*, *Bio/Technology* (1988) 6:47-55, Miller *et al.*, *Generic Engineering* (1986) 8:277-279, and Maeda *et al.*, *Nature* (1985) 315:592-594.

Mammalian Cells. Mammalian expression is accomplished as described in Dijkema *et al.*, *EMBO J.* (1985) 4:761, Gorman *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1982) 79:6777, Boshart *et al.*, *Cell* (1985) 41:521 and U.S. Patent No. 4,399,216. Other features of mammalian expression are facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) 58:44, Barnes and Sato, *Anal. Biochem.* (1980) 102:255, U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence inserted into the genome of the cell at location sufficient to at least enhance expressed of the gene in the cell. The regulatory sequence may be designed to integrate into the genome via homologous recombination, as disclosed in U.S. Patent Nos. 5,641,670 and 5,733,761, the disclosures of which are herein incorporated by reference, or may be designed to integrate into the genome via non-homologous recombination, as described in WO 99/15650, the disclosure of which is herein incorporated by reference. As such, also encompassed in the subject invention is the production of the subject proteins without manipulation of the encoding nucleic acid itself, but instead through

integration of a regulatory sequence into the genome of cell that already includes a gene encoding the desired protein, as described in the above incorporated patent documents.

Also provided are homologs of the subject nucleic acids. Homologs are identified by any of a number of methods. A fragment of the provided cDNA may be used as a hybridization probe against a cDNA library from the target organism of interest, where low stringency conditions are used. The probe may be a large fragment, or one or more short degenerate primers. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 6×SSC (0.9 M sodium chloride/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1×SSC (0.15 M sodium chloride/0.15 M sodium citrate). Sequence identity may be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1×SSC (15 mM sodium chloride/1.5 mM sodium citrate). Nucleic acids having a region of substantial identity to the provided sequences, e.g. allelic variants, genetically altered versions of the gene, etc., bind to the provided sequences under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes.

Also of interest are promoter elements of the subject genomic sequences, where the sequence of the 5' flanking region may be utilized for promoter elements, including enhancer binding sites, e.g., that provide for regulation of expression in cells/tissues where the subject proteins gene are expressed.

Also provided are small DNA fragments of the subject nucleic acids, which fragments are useful as primers for PCR, hybridization screening probes, etc. Larger DNA fragments, *i.e.*, greater than 100 nt are useful for production of the encoded polypeptide, as described in the previous section. For use in geometric amplification reactions, such as geometric PCR, a pair of primers will be used. The exact composition of the primer sequences is not critical to the invention, but for most applications the primers will hybridize to the subject sequence under stringent conditions, as known in the art. It is preferable to choose a pair of primers that will generate an amplification product of at least about 50 nt, preferably at least about 100 nt. Algorithms for the selection of primer sequences are generally known, and are available in commercial software packages.

Amplification primers hybridize to complementary strands of DNA, and will prime towards each other.

The DNA may also be used to identify expression of the gene in a biological specimen. The manner in which one probes cells for the presence of particular nucleotide sequences, as genomic DNA or RNA, is well established in the literature. Briefly, DNA or mRNA is isolated from a cell sample. The mRNA may be amplified by RT-PCR, using reverse transcriptase to form a complementary DNA strand, followed by polymerase chain reaction amplification using primers specific for the subject DNA sequences. Alternatively, the mRNA sample is separated by gel electrophoresis, transferred to a suitable support, *e.g.* nitrocellulose, nylon, *etc.*, and then probed with a fragment of the subject DNA as a probe. Other techniques, such as oligonucleotide ligation assays, *in situ* hybridizations, and hybridization to DNA probes arrayed on a solid chip may also find use. Detection of mRNA hybridizing to the subject sequence is indicative of Anthozoan protein gene expression in the sample.

The subject nucleic acids, including flanking promoter regions and coding regions, may be mutated in various ways known in the art to generate targeted changes in promoter strength, sequence of the encoded protein, properties of the encoded protein, including fluorescent properties of the encoded protein, *etc.* The DNA sequence or protein product of such a mutation will usually be substantially similar to the sequences provided herein, *e.g.* will differ by at least one nucleotide or amino acid, respectively, and may differ by at least two but not more than about ten nucleotides or amino acids. The sequence changes may be substitutions, insertions, deletions, or a combination thereof. Deletions may further include larger changes, such as deletions of a domain or exon, *e.g.* of stretches of 10, 20, 50, 75, 100, 150 or more aa residues. Techniques for *in vitro* mutagenesis of cloned genes are known. Examples of protocols for site specific mutagenesis may be found in Gustin *et al.* (1993), *Biotechniques* 14:22; Barany (1985), *Gene* 37:111-23; Colicelli *et al.* (1985), *Mol. Gen. Genet.* 199:537-9; and Prentki *et al.* (1984), *Gene* 29:303-13. Methods for site specific mutagenesis can be found in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, CSH Press 1989, pp. 15.3-15.108; Weiner *et al.* (1993), *Gene* 126:35-41; Sayers *et al.* (1992), *Biotechniques* 13:592-6; Jones and Winistorfer (1992), *Biotechniques* 12:528-30;

Barton *et al.* (1990), *Nucleic Acids Res* 18:7349-55; Marotti and Tomich (1989), *Gene Anal. Tech.* 6:67-70; and Zhu (1989), *Anal Biochem* 177:120-4. Such mutated nucleic acid derivatives may be used to study structure-function relationships of a particular chromo/ fluorescent protein, or to alter properties of the protein that affect its function or regulation.

Of particular interest in many embodiments is the following specific mutation protocol, which protocol finds use in mutating chromoproteins (e.g., colored proteins that have little if any fluorescence) into fluorescent mutants. In this protocol, the sequence of the candidate protein is aligned with the amino acid sequence of *Aequorea victoria* wild type GFP, according to the protocol reported in Matz *et al.*, "Fluorescent proteins from non-bioluminescent Anthozoa species," *Nature Biotechnology* (October 1999) 17: 969 –973. Residue 148 of the aligned chromoprotein is identified and then changed to Ser, e.g., by site directed mutagenesis, which results in the production of a fluorescent mutant of the wild type chromoprotein. See e.g., NFP-7 described below, which wild type protein is a chromoprotein that is mutated into a fluorescent protein by substitution of Ser for the native Ala residue at position 148.

Also of interest are humanized versions of the subject nucleic acids. As used herein, the term "humanized" refers to changes made to the a nucleic acid sequence to optimize the codons for expression of the protein in human cells (Yang *et al.*, *Nucleic Acids Research* 24 (1996), 4592-4593). See also U.S. Patent No. 5,795,737 which describes humanization of proteins, the disclosure of which is herein incorporated by reference.

PROTEIN/POLYPEPTIDE COMPOSITIONS

Also provided by the subject invention are chromo- and/or fluorescent proteins and mutants thereof, as well as polypeptide compositions related thereto. As the subject proteins are chromoproteins, they are colored proteins, which may be fluorescent, low or non- fluorescent. As used herein, the terms chromoprotein and fluorescent protein do not include luciferases, such as Renilla luciferase, and refer to any protein that is pigmented or colored and/or fluoresces when irradiated with light, e.g., white light or light of a specific wavelength (or narrow band of

wavelengths such as an excitation wavelength). The term polypeptide composition as used herein refers to both the full-length protein, as well as portions or fragments thereof. Also included in this term are variations of the naturally occurring protein, where such variations are homologous or substantially similar to the naturally occurring protein, and mutants of the naturally occurring proteins, as described in greater detail below. The subject polypeptides are present in other than their natural environment.

In many embodiments, the subject proteins have an absorbance maximum ranging from about 300 to 700, usually from about 350 to 650 and more usually from about 400 to 600 nm. Where the subject proteins are fluorescent proteins, by which is meant that they can be excited at one wavelength of light following which they will emit light at another wavelength, the excitation spectra of the subject proteins typically ranges from about 300 to 700, usually from about 350 to 650 and more usually from about 400 to 600 nm while the emission spectra of the subject proteins typically ranges from about 400 to 800, usually from about 425 to 775 and more usually from about 450 to 750 nm. The subject proteins generally have a maximum extinction coefficient that ranges from about 10,000 to 50,000 and usually from about 15,000 to 45,000. The subject proteins typically range in length from about 150 to 300 and usually from about 200 to 300 amino acid residues; and generally have a molecular weight ranging from about 15 to 35 kDa, usually from about 17.5 to 32.5 kDa.

In certain embodiments, the subject proteins are bright, where by bright is meant that the chromoproteins and their fluorescent mutants can be detected by common methods (e.g., visual screening, spectrophotometry, spectrofluorometry, fluorescent microscopy, by FACS machines, etc.) Fluorescence brightness of particular fluorescent proteins is determined by its quantum yield multiplied by maximal extinction coefficient. Brightness of a chromoproteins may be expressed by its maximal extinction coefficient.

In certain embodiments, the subject proteins fold rapidly following expression in the host cell. By rapidly folding is meant that the proteins achieve their tertiary structure that gives rise to their chromo- or fluorescent quality in a short period of time. In these embodiments, the proteins fold in a period of time that generally does not exceed about 3 days, usually does not exceed about 2 days and more usually does not exceed about 1 day.

Specific proteins of interest include the following specific proteins: (1) Green fluorescent protein from *Heteractis crispa* (hcriGFP); (2) Green fluorescent protein from *Dendronephthya* sp. (dendGFP); (3) Red fluorescent protein from *Zoanthus* sp. (zoanRFP); (4) Green fluorescent protein from *Scolymia cubensis* (scubGFP1);

5 (5) Green fluorescent protein from *Scolymia cubensis* (scubGFP2); (6) Red fluorescent protein from *Ricordea florida* (rfloRFP); (7) Green fluorescent protein from *Ricordea florida* (rfloGFP); (8) Red fluorescent protein from *Montastraea cavernosa* (mcavRFP); (9) Green fluorescent protein from *Montastraea cavernosa* (mcavGFP); (10) Green fluorescent protein from *Condylactis gigantea* (cgigGFP);

10 (11) Green fluorescent protein from *Agaricia fragilis* (afraGFP); (12) Green fluorescent protein from *Ricordea florida* (rfloGFP2); (13) Green fluorescent protein from *Montastraea cavernosa* (mcavGFP2); and (14) Green fluorescent protein homolog from *Montastraea annularis* (mannFP).

Homologs or proteins (or fragments thereof) that vary in sequence from the

15 above provided specific amino acid sequences of the subject invention, i.e., SEQ ID NOS: 02; 04; 06; 08; 10; 12; 14; 16; 18; 20; 22; 24; 26 or 28, are also provided. By homolog is meant a protein having at least about 10%, usually at least about 20 % and more usually at least about 30 %, and in many embodiments at least about 35 %, usually at least about 40% and more usually at least about 60 %

20 amino acid sequence identity to the protein of the subject invention, as determined using MegAlign, DNASTAR (1998) clustal algorithm as described in D. G. Higgins and P.M. Sharp, "Fast and Sensitive multiple Sequence Alignments on a Microcomputer," (1989) CABIOS, 5: 151-153. (Parameters used are ktuple 1, gap penalty 3, window, 5 and diagonals saved 5). In many embodiments, homologues

25 of interest have much higher sequence identify, e.g., 65%, 70%, 75%, 80%, 85%, 90% or higher.

Also provided are proteins that are substantially identical to the wild type protein, where by substantially identical is meant that the protein has an amino acid sequence identity to the sequence of wild type protein of at least about 60%,

30 usually at least about 65% and more usually at least about 70 %, where in some instances the identity may be much higher, e.g., 75%, 80%, 85%, 90%, 95% or higher.

In many embodiments, the subject homologues have structural features found in the above provided specific sequences, where such structural features include the β -can fold.

Proteins which are mutants of the above-described naturally occurring proteins are also provided. Mutants may retain biological properties of the wild-type (e.g., naturally occurring) proteins, or may have biological properties which differ from the wild-type proteins. The term "biological property" of the subject proteins includes, but is not limited to, spectral properties, such as absorbance maximum, emission maximum, maximum extinction coefficient, brightness (e.g., as compared to the wild-type protein or another reference protein such as green fluorescent protein from *A. victoria*), and the like; *in vivo* and/or *in vitro* stability (e.g., half-life); etc. Mutants include single amino acid changes, deletions of one or more amino acids, N-terminal truncations, C-terminal truncations, insertions, etc.

Mutants can be generated using standard techniques of molecular biology, e.g., random mutagenesis, and targeted mutagenesis. Several mutants are described herein. Given the guidance provided in the Examples, and using standard techniques, those skilled in the art can readily generate a wide variety of additional mutants and test whether a biological property has been altered. For example, fluorescence intensity can be measured using a spectrophotometer at various excitation wavelengths.

Those proteins of the subject invention that are naturally occurring proteins are present in a non-naturally occurring environment, e.g., are separated from their naturally occurring environment. In certain embodiments, the subject proteins are present in a composition that is enriched for the subject protein as compared to its naturally occurring environment. For example, purified protein is provided, where by purified is meant that the protein is present in a composition that is substantially free of non- chromo/fluoroprotein proteins of interest, where by substantially free is meant that less than 90 %, usually less than 60 % and more usually less than 50 % of the composition is made up of non- chromoproteins or mutants thereof of interest. The proteins of the subject invention may also be present as an isolate, by which is meant that the protein is substantially free of other proteins and other naturally occurring biologic molecules, such as

oligosaccharides, polynucleotides and fragments thereof, and the like, where the term "substantially free" in this instance means that less than 70 %, usually less than 60% and more usually less than 50 % of the composition containing the isolated protein is some other naturally occurring biological molecule. In certain
5 embodiments, the proteins are present in substantially pure form, where by "substantially pure form" is meant at least 95%, usually at least 97% and more usually at least 99% pure.

In addition to the naturally occurring proteins, polypeptides that vary from the naturally occurring proteins, e.g., the mutant proteins described above, are
10 also provided. Generally such polypeptides include an amino acid sequence encoded by an open reading frame (ORF) of the gene encoding the subject wild type protein, including the full length protein and fragments thereof, particularly biologically active fragments and/or fragments corresponding to functional domains, and the like; and including fusions of the subject polypeptides to other
15 proteins or parts thereof. Fragments of interest will typically be at least about 10 aa in length, usually at least about 50 aa in length, and may be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to the subject protein of at least about 10 aa, and usually at least about 15 aa, and in many embodiments
20 at least about 50 aa in length. In some embodiments, the subject polypeptides are about 25 aa, about 50 aa, about 75 aa, about 100 aa, about 125 aa, about 150 aa, about 200 aa, about 210 aa, about 220 aa, about 230 aa, or about 240 aa in length, up to the entire protein. In some embodiments, a protein fragment retains all or substantially all of a biological property of the wild-type protein.

25 The subject proteins and polypeptides may be obtained from naturally occurring sources or synthetically produced. For example, wild type proteins may be derived from biological sources which express the proteins, e.g., non-bioluminescent Cnidarian, e.g., Anthozoan, species, such as the specific ones listed above. The subject proteins may also be derived from synthetic means, e.g.,
30 by expressing a recombinant gene or nucleic acid coding sequence encoding the protein of interest in a suitable host, as described above. Any convenient protein purification procedures may be employed, where suitable protein purification methodologies are described in Guide to Protein Purification, (Deuthser ed.) (Academic Press, 1990). For example, a lysate may prepared from the original

source and purified using HPLC, exclusion chromatography, gel electrophoresis, affinity chromatography, and the like.

ANTIBODY COMPOSITIONS

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Also provided are antibodies that specifically bind to the subject fluorescent proteins. Suitable antibodies are obtained by immunizing a host animal with peptides comprising all or a portion of the subject protein. Suitable host animals include mouse, rat sheep, goat, hamster, rabbit, *etc.* The origin of the protein
10 immunogen will generally be a Cnidarian species, specifically a non-bioluminescent Cnidarian species, such as an Anthozoan species or a non-Petallucean Anthozoan species. The host animal will generally be a different species than the immunogen, *e.g.*, mice, *etc.*

The immunogen may comprise the complete protein, or fragments and
15 derivatives thereof. Preferred immunogens comprise all or a part of the protein, where these residues contain the post-translation modifications found on the native target protein. Immunogens are produced in a variety of ways known in the art, *e.g.*, expression of cloned genes using conventional recombinant methods, isolation from Anthozoan species of origin, *etc.*

20 For preparation of polyclonal antibodies, the first step is immunization of the host animal with the target protein, where the target protein will preferably be in substantially pure form, comprising less than about 1% contaminant. The immunogen may comprise the complete target protein, fragments or derivatives thereof. To increase the immune response of the host animal, the target protein
25 may be combined with an adjuvant, where suitable adjuvants include alum, dextran, sulfate, large polymeric anions, oil & water emulsions, *e.g.* Freund's adjuvant, Freund's complete adjuvant, and the like. The target protein may also be conjugated to synthetic carrier proteins or synthetic antigens. A variety of hosts may be immunized to produce the polyclonal antibodies. Such hosts include
30 rabbits, guinea pigs, rodents, *e.g.* mice, rats, sheep, goats, and the like. The target protein is administered to the host, usually intradermally, with an initial dosage followed by one or more, usually at least two, additional booster dosages. Following immunization, the blood from the host will be collected, followed by

separation of the serum from the blood cells. The Ig present in the resultant antiserum may be further fractionated using known methods, such as ammonium salt fractionation, DEAE chromatography, and the like.

Monoclonal antibodies are produced by conventional techniques. Generally, the spleen and/or lymph nodes of an immunized host animal provide a source of plasma cells. The plasma cells are immortalized by fusion with myeloma cells to produce hybridoma cells. Culture supernatant from individual hybridomas is screened using standard techniques to identify those producing antibodies with the desired specificity. Suitable animals for production of monoclonal antibodies to the human protein include mouse, rat, hamster, *etc.* To raise antibodies against the mouse protein, the animal will generally be a hamster, guinea pig, rabbit, *etc.* The antibody may be purified from the hybridoma cell supernatants or ascites fluid by conventional techniques, *e.g.* affinity chromatography using protein bound to an insoluble support, protein A sepharose, *etc.*

The antibody may be produced as a single chain, instead of the normal multimeric structure. Single chain antibodies are described in Jost *et al.* (1994) J.B.C. 269:26267-73, and others. DNA sequences encoding the variable region of the heavy chain and the variable region of the light chain are ligated to a spacer encoding at least about 4 amino acids of small neutral amino acids, including glycine and/or serine. The protein encoded by this fusion allows assembly of a functional variable region that retains the specificity and affinity of the original antibody.

Also of interest in certain embodiments are humanized antibodies. Methods of humanizing antibodies are known in the art. The humanized antibody may be the product of an animal having transgenic human immunoglobulin constant region genes (see for example International Patent Applications WO 90/10077 and WO 90/04036). Alternatively, the antibody of interest may be engineered by recombinant DNA techniques to substitute the CH1, CH2, CH3, hinge domains, and/or the framework domain with the corresponding human sequence (see WO 92/02190).

The use of Ig cDNA for construction of chimeric immunoglobulin genes is known in the art (Liu *et al.* (1987) P.N.A.S. 84:3439 and (1987) J. Immunol. 139:3521). mRNA is isolated from a hybridoma or other cell producing the

antibody and used to produce cDNA. The cDNA of interest may be amplified by the polymerase chain reaction using specific primers (U.S. Patent nos. 4,683,195 and 4,683,202). Alternatively, a library is made and screened to isolate the sequence of interest. The DNA sequence encoding the variable region of the antibody is then fused to human constant region sequences. The sequences of human constant regions genes may be found in Kabat *et al.* (1991) Sequences of Proteins of Immunological Interest, N.I.H. publication no. 91-3242. Human C region genes are readily available from known clones. The choice of isotype will be guided by the desired effector functions, such as complement fixation, or activity in antibody-dependent cellular cytotoxicity. Preferred isotypes are IgG1, IgG3 and IgG4. Either of the human light chain constant regions, kappa or lambda, may be used. The chimeric, humanized antibody is then expressed by conventional methods.

Antibody fragments, such as Fv, F(ab')₂ and Fab may be prepared by cleavage of the intact protein, e.g. by protease or chemical cleavage. Alternatively, a truncated gene is designed. For example, a chimeric gene encoding a portion of the F(ab')₂ fragment would include DNA sequences encoding the CH1 domain and hinge region of the H chain, followed by a translational stop codon to yield the truncated molecule.

Consensus sequences of H and L J regions may be used to design oligonucleotides for use as primers to introduce useful restriction sites into the J region for subsequent linkage of V region segments to human C region segments. C region cDNA can be modified by site directed mutagenesis to place a restriction site at the analogous position in the human sequence.

Expression vectors include plasmids, retroviruses, YACs, EBV derived episomes, and the like. A convenient vector is one that encodes a functionally complete human CH or CL immunoglobulin sequence, with appropriate restriction sites engineered so that any VH or VL sequence can be easily inserted and expressed. In such vectors, splicing usually occurs between the splice donor site in the inserted J region and the splice acceptor site preceding the human C region, and also at the splice regions that occur within the human CH exons. Polyadenylation and transcription termination occur at native chromosomal sites downstream of the coding regions. The resulting chimeric antibody may be joined

to any strong promoter, including retroviral LTRs, *e.g.* SV-40 early promoter, (Okayama *et al.* (1983) Mol. Cell. Bio. 3:280), Rous sarcoma virus LTR (Gorman *et al.* (1982) P.N.A.S. 79:6777), and moloney murine leukemia virus LTR (Grosschedl *et al.* (1985) Cell 41:885); native Ig promoters, *etc.*

5

TRANSGENICS

The subject nucleic acids can be used to generate transgenic, non-human plants or animals or site specific gene modifications in cell lines. Transgenic cells of the subject invention include one or more nucleic acids according to the subject invention present as a transgene, where included within this definition are the parent cells transformed to include the transgene and the progeny thereof. In many embodiments, the transgenic cells are cells that do not normally harbor or contain a nucleic acid according to the subject invention. In those embodiments where the transgenic cells do not naturally contain the subject nucleic acids, the nucleic acid will be present in the cell in a position other than its natural location, *i.e.* integrated into the genomic material of the cell at a non-natural location.

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Transgenic animals may be made through homologous recombination, where the endogenous locus is altered. Alternatively, a nucleic acid construct is randomly integrated into the genome. Vectors for stable integration include plasmids, retroviruses and other animal viruses, YACs, and the like.

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Transgenic organisms of the subject invention include cells and multicellular organisms, *e.g.*, plants and animals, that are endogenous knockouts in which expression of the endogenous gene is at least reduced if not eliminated. Transgenic organisms of interest also include cells and multicellular organisms, *e.g.*, plants and animals, in which the protein or variants thereof is expressed in cells or tissues where it is not normally expressed and/or at levels not normally present in such cells or tissues.

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DNA constructs for homologous recombination will comprise at least a portion of the gene of the subject invention, wherein the gene has the desired genetic modification(s), and includes regions of homology to the target locus. DNA constructs for random integration need not include regions of homology to mediate recombination. Conveniently, markers for positive and negative selection are included. Methods for generating cells having targeted gene modifications

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through homologous recombination are known in the art. For various techniques for transfecting mammalian cells, see Keown *et al.* (1990), *Meth. Enzymol.* 185:527-537.

For embryonic stem (ES) cells, an ES cell line may be employed, or
5 embryonic cells may be obtained freshly from a host, e.g. mouse, rat, guinea pig, etc. Such cells are grown on an appropriate fibroblast-feeder layer or grown in the presence of leukemia inhibiting factor (LIF). When ES or embryonic cells have been transformed, they may be used to produce transgenic animals. After transformation, the cells are plated onto a feeder layer in an appropriate medium.
10 Cells containing the construct may be detected by employing a selective medium. After sufficient time for colonies to grow, they are picked and analyzed for the occurrence of homologous recombination or integration of the construct. Those colonies that are positive may then be used for embryo manipulation and blastocyst injection. Blastocysts are obtained from 4 to 6 week old superovulated
15 females. The ES cells are trypsinized, and the modified cells are injected into the blastocoel of the blastocyst. After injection, the blastocysts are returned to each uterine horn of pseudopregnant females. Females are then allowed to go to term and the resulting offspring screened for the construct. By providing for a different phenotype of the blastocyst and the genetically modified cells, chimeric progeny
20 can be readily detected.

The chimeric animals are screened for the presence of the modified gene and males and females having the modification are mated to produce homozygous progeny. If the gene alterations cause lethality at some point in development, tissues or organs can be maintained as allogeneic or congenic
25 grafts or transplants, or in *in vitro* culture. The transgenic animals may be any non-human mammal, such as laboratory animals, domestic animals, etc. The transgenic animals may be used in functional studies, drug screening, etc. Representative examples of the use of transgenic animals include those described
infra.

30 Transgenic plants may be produced in a similar manner. Methods of preparing transgenic plant cells and plants are described in U.S. Pat. Nos. 5,767,367; 5,750,870; 5,739,409; 5,689,049; 5,689,045; 5,674,731; 5,656,466; 5,633,155; 5,629,470 ; 5,595,896; 5,576,198; 5,538,879; 5,484,956; the

disclosures of which are herein incorporated by reference. Methods of producing transgenic plants are also reviewed in Plant Biochemistry and Molecular Biology (eds Lea & Leegood, John Wiley & Sons)(1993) pp 275-295. In brief, a suitable plant cell or tissue is harvested, depending on the nature of the plant species. As such, in certain instances, protoplasts will be isolated, where such protoplasts may be isolated from a variety of different plant tissues, e.g. leaf, hypocotyl, root, etc. For protoplast isolation, the harvested cells are incubated in the presence of cellulases in order to remove the cell wall, where the exact incubation conditions vary depending on the type of plant and/or tissue from which the cell is derived. The resultant protoplasts are then separated from the resultant cellular debris by sieving and centrifugation. Instead of using protoplasts, embryogenic explants comprising somatic cells may be used for preparation of the transgenic host. Following cell or tissue harvesting, exogenous DNA of interest is introduced into the plant cells, where a variety of different techniques are available for such introduction. With isolated protoplasts, the opportunity arise for introduction via DNA-mediated gene transfer protocols, including: incubation of the protoplasts with naked DNA, e.g. plasmids, comprising the exogenous coding sequence of interest in the presence of polyvalent cations, e.g. PEG or PLO; and electroporation of the protoplasts in the presence of naked DNA comprising the exogenous sequence of interest. Protoplasts that have successfully taken up the exogenous DNA are then selected, grown into a callus, and ultimately into a transgenic plant through contact with the appropriate amounts and ratios of stimulatory factors, e.g. auxins and cytokinins. With embryogenic explants, a convenient method of introducing the exogenous DNA in the target somatic cells is through the use of particle acceleration or "gene-gun" protocols. The resultant explants are then allowed to grow into chimera plants, cross-bred and transgenic progeny are obtained. Instead of the naked DNA approaches described above, another convenient method of producing transgenic plants is *Agrobacterium* mediated transformation. With *Agrobacterium* mediated transformation, co-integrative or binary vectors comprising the exogenous DNA are prepared and then introduced into an appropriate *Agrobacterium* strain, e.g. *A. tumefaciens*. The resultant bacteria are then incubated with prepared protoplasts or tissue explants, e.g. leaf disks, and a callus is produced. The callus is then grown under selective

conditions, selected and subjected to growth media to induce root and shoot growth to ultimately produce a transgenic plant.

UTILITY

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The subject chromoproteins and fluorescent mutants thereof find use in a variety of different applications, where the applications necessarily differ depending on whether the protein is a chromoprotein or a fluorescent protein. Representative uses for each of these types of proteins will be described below, where the follow described uses are merely representative and are in no way meant to limit the use of the subject proteins to those described below.

Chromoproteins

15 The subject chromoproteins of the present invention find use in a variety of different applications. One application of interest is the use of the subject proteins as coloring agents which are capable of imparting color or pigment to a particular composition of matter. Of particular interest in certain embodiments are non-toxic chromoproteins. The subject chromoproteins may be incorporated into a variety of
20 different compositions of matter, where representative compositions of matter include: food compositions, pharmaceuticals, cosmetics, living organisms, e.g., animals and plants, and the like. Where used as a coloring agent or pigment, a sufficient amount of the chromoprotein is incorporated into the composition of matter to impart the desired color or pigment thereto. The chromoprotein may be
25 incorporated into the composition of matter using any convenient protocol, where the particular protocol employed will necessarily depend, at least in part, on the nature of the composition of matter to be colored. Protocols that may be employed include, but are not limited to: blending, diffusion, friction, spraying, injection, tattooing, and the like.

30 The chromoproteins may also find use as labels in analyte detection assays, e.g., assays for biological analytes of interest. For example, the chromoproteins may be incorporated into adducts with analyte specific antibodies or binding fragments thereof and subsequently employed in immunoassays for

analytes of interest in a complex sample, as described in U.S. Patent No. 4,302,536; the disclosure of which is herein incorporated by reference. Instead of antibodies or binding fragments thereof, the subject chromoproteins or chromogenic fragments thereof may be conjugated to ligands that specifically bind to an analyte of interest, or other moieties, growth factors, hormones, and the like; as is readily apparent to those of skill in the art.

In yet other embodiments, the subject chromoproteins may be used as selectable markers in recombinant DNA applications, e.g., the production of transgenic cells and organisms, as described above. As such, one can engineer a particular transgenic production protocol to employ expression of the subject chromoproteins as a selectable marker, either for a successful or unsuccessful protocol. Thus, appearance of the color of the subject chromoprotein in the phenotype of the transgenic organism produced by a particular process can be used to indicate that the particular organism successfully harbors the transgene of interest, often integrated in a manner that provides for expression of the transgene in the organism. When used a selectable marker, a nucleic acid encoding for the subject chromoprotein can be employed in the transgenic generation process, where this process is described in greater detail supra. Particular transgenic organisms of interest where the subject proteins may be employed as selectable markers include transgenic plants, animals, bacteria, fungi, and the like.

In yet other embodiments, the chromoproteins (and fluorescent proteins) of the subject invention find use in sunscreens, as selective filters, etc., in a manner similar to the uses of the proteins described in WO 00/46233.

Fluorescent Proteins

The subject fluorescent proteins of the present invention (as well as other components of the subject invention described above) find use in a variety of different applications, where such applications include, but are not limited to, the following. The first application of interest is the use of the subject proteins in fluorescence resonance energy transfer (FRET) applications. In these applications, the subject proteins serve as donor and/or acceptors in combination with a second fluorescent protein or dye, e.g., a fluorescent protein as described in

Matz et al., *Nature Biotechnology* (October 1999) 17:969-973, a green fluorescent protein from *Aequoria victoria* or fluorescent mutant thereof, e.g., as described in U.S. Patent No. 6,066,476; 6,020,192; 5,985,577; 5,976,796; 5,968,750; 5,968,738; 5,958,713; 5,919,445; 5,874,304, the disclosures of which are herein
5 incorporated by reference, other fluorescent dyes, e.g., coumarin and its derivatives, e.g. 7-amino-4-methylcoumarin, aminocoumarin, bodipy dyes, such as Bodipy FL, cascade blue, fluorescein and its derivatives, e.g. fluorescein isothiocyanate, Oregon green, rhodamine dyes, e.g. texas red, tetramethylrhodamine, eosins and erythrosins, cyanine dyes, e.g. Cy3 and Cy5,
10 macrocyclic chelates of lanthanide ions, e.g. quantum dye, etc., chemiluminescent dyes, e.g., luciferases, including those described in U.S. Patent Nos. 5,843,746; 5,700,673; 5,674,713; 5,618,722; 5,418,155; 5,330,906; 5,229,285; 5,221,623; 5,182,202; the disclosures of which are herein incorporated by reference. Specific examples of where FRET assays employing the subject fluorescent proteins may
15 be used include, but are not limited to: the detection of protein-protein interactions, e.g., mammalian two-hybrid system, transcription factor dimerization, membrane protein multimerization; multiprotein complex formation, etc., as a biosensor for a number of different events, where a peptide or protein covalently links a FRET fluorescent combination including the subject fluorescent proteins and the linking
20 peptide or protein is, e.g., a protease specific substrate, e.g., for caspase mediated cleavage, a linker that undergoes conformational change upon receiving a signal which increases or decreases FRET, e.g., PKA regulatory domain (cAMP-sensor), phosphorylation, e.g., where there is a phosphorylation site in the linker or the linker has binding specificity to phosphorylated/dephosphorylated domain of
25 another protein, or the linker has Ca^{2+} binding domain. Representative fluorescence resonance energy transfer or FRET applications in which the subject proteins find use include, but are not limited to, those described in: U.S. Patent Nos. 6,008,373; 5,998,146; 5,981,200; 5,945,526; 5,945,283; 5,911,952; 5,869,255; 5,866,336; 5,863,727; 5,728,528; 5,707,804; 5,688,648; 5,439,797; the
30 disclosures of which are herein incorporated by reference.

The subject fluorescent proteins also find use as biosensors in prokaryotic and eukaryotic cells, e.g. as Ca^{2+} ion indicator; as pH indicator, as phosphorylation indicator, as an indicator of other ions, e.g., magnesium, sodium, potassium, chloride and halides. For example, for detection of Ca ion, proteins containing an

EF-hand motifs are known to translocate from the cytosol to membranes upon Ca^{2+} binding. These proteins contain a myristoyl group that is buried within the molecule by hydrophobic interactions with other regions of the protein. Binding of Ca^{2+} induces a conformational change exposing the myristoyl group which then is available for the insertion into the lipid bilayer (called a " Ca^{2+} -myristoyl switch"). Fusion of such a EF-hand containing protein to Fluorescent Proteins (FP) could make it an indicator of intracellular Ca^{2+} by monitoring the translocation from the cytosol to the plasma membrane by confocal microscopy. EF-hand proteins suitable for use in this system include, but are not limited to: recoverin (1-3), calcineurin B, troponin C, visinin, neurocalcin, calmodulin, parvalbumin, and the like. For pH, a system based on hisactophilins may be employed. Hisactophilins are myristoylated histidine-rich proteins known to exist in *Dictyostelium*. Their binding to actin and acidic lipids is sharply pH-dependent within the range of cytoplasmic pH variations. In living cells membrane binding seems to override the interaction of hisactophilins with actin filaments. At $\text{pH} \leq 6.5$ they locate to the plasma membrane and nucleus. In contrast, at pH 7.5 they evenly distribute throughout the cytoplasmic space. This change of distribution is reversible and is attributed to histidine clusters exposed in loops on the surface of the molecule. The reversion of intracellular distribution in the range of cytoplasmic pH variations is in accord with a pK of 6.5 of histidine residues. The cellular distribution is independent of myristoylation of the protein. By fusing FPs (Fluorescent Proteins) to hisactophilin the intracellular distribution of the fusion protein can be followed by laser scanning, confocal microscopy or standard fluorescence microscopy. Quantitative fluorescence analysis can be done by performing line scans through cells (laser scanning confocal microscopy) or other electronic data analysis (e.g., using metamorph software (Universal Imaging Corp) and averaging of data collected in a population of cells. Substantial pH-dependent redistribution of hisactophilin-FP from the cytosol to the plasma membrane occurs within 1-2 min and reaches a steady state level after 5-10 min. The reverse reaction takes place on a similar time scale. As such, hisactophilin-fluorescent protein fusion protein that acts in an analogous fashion can be used to monitor cytosolic pH changes in real time in live mammalian cells. Such methods have use in high throughput applications, e.g., in the measurement of pH changes as consequence of growth factor receptor activation (e.g. epithelial or platelet-derived growth factor)

chemotactic stimulation/ cell locomotion, in the detection of intracellular pH changes as second messenger, in the monitoring of intracellular pH in pH manipulating experiments, and the like. For detection of PKC activity, the reporter system exploits the fact that a molecule called MARCKS (myristoylated alanine-rich C kinase substrate) is a PKC substrate. It is anchored to the plasma membrane via myristoylation and a stretch of positively charged amino acids (ED-domain) that bind to the negatively charged plasma membrane via electrostatic interactions. Upon PKC activation the ED-domain becomes phosphorylated by PKC, thereby becoming negatively charged, and as a consequence of electrostatic repulsion MARCKS translocates from the plasma membrane to the cytoplasm (called the "myristoyl-electrostatic switch"). Fusion of the N-terminus of MARCKS ranging from the myristoylation motif to the ED-domain of MARCKS to fluorescent proteins of the present invention makes the above a detector system for PKC activity. When phosphorylated by PKC, the fusion protein translocates from the plasma membrane to the cytosol. This translocation is followed by standard fluorescence microscopy or confocal microscopy e.g. using the Cellomics technology or other High Content Screening systems (e.g. Universal Imaging Corp./Becton Dickinson). The above reporter system has application in High Content Screening, e.g., screening for PKC inhibitors, and as an indicator for PKC activity in many screening scenarios for potential reagents interfering with this signal transduction pathway. Methods of using fluorescent proteins as biosensors also include those described in U.S. Patent Nos. 972,638; 5,824,485 and 5,650,135 (as well as the references cited therein) the disclosures of which are herein incorporated by reference.

The subject fluorescent proteins also find use in applications involving the automated screening of arrays of cells expressing fluorescent reporting groups by using microscopic imaging and electronic analysis. Screening can be used for drug discovery and in the field of functional genomics: e.g., where the subject proteins are used as markers of whole cells to detect changes in multicellular reorganization and migration, e.g., formation of multicellular tubules (blood vessel formation) by endothelial cells, migration of cells through Fluoroblok Insert System (Becton Dickinson Co.), wound healing, neurite outgrowth, etc.; where the proteins are used as markers fused to peptides (e.g., targeting sequences) and proteins that allow the detection of change of intracellular location as indicator for cellular

activity, for example: signal transduction, such as kinase and transcription factor translocation upon stimuli, such as protein kinase C, protein kinase A, transcription factor NFkB, and NFAT; cell cycle proteins, such as cyclin A, cyclin B1 and cyclinE; protease cleavage with subsequent movement of cleaved substrate, phospholipids, with markers for intracellular structures such as endoplasmic reticulum, Golgi apparatus, mitochondria, peroxisomes, nucleus, nucleoli, plasma membrane, histones, endosomes, lysosomes, microtubules, actin) as tools for High Content Screening: co-localization of other fluorescent fusion proteins with these localization markers as indicators of movements of intracellular fluorescent fusion proteins/peptides or as marker alone; and the like. Examples of applications involving the automated screening of arrays of cells in which the subject fluorescent proteins find use include: U.S. Patent No. 5,989,835; as well as WO/0017624; WO 00/26408; WO 00/17643; and WO 00/03246; the disclosures of which are herein incorporated by reference.

The subject fluorescent proteins also find use in high through-put screening assays. The subject fluorescent proteins are stable proteins with half-lives of more than 24h. Also provided are destabilized versions of the subject fluorescent proteins with shorter half-lives that can be used as transcription reporters for drug discovery. For example, a protein according to the subject invention can be fused with a putative proteolytic signal sequence derived from a protein with shorter half-life, e.g., PEST sequence from the mouse ornithine decarboxylase gene, mouse cyclin B1 destruction box and ubiquitin, etc. For a description of destabilized proteins and vectors that can be employed to produce the same, see e.g., U.S. Patent No. 6,130,313; the disclosure of which is herein incorporated by reference. Promoters in signal transduction pathways can be detected using destabilized versions of the subject fluorescent proteins for drug screening, e.g., AP1, NFAT, NFkB, Smad, STAT, p53, E2F, Rb, myc, CRE, ER, GR and TRE, and the like.

The subject proteins can be used as second messenger detectors, e.g., by fusing the subject proteins to specific domains: e.g., PKCgamma Ca binding domain, PKCgamma DAG binding domain, SH2 domain and SH3 domain, etc.

Secreted forms of the subject proteins can be prepared, e.g. by fusing secreted leading sequences to the subject proteins to construct secreted forms of the subject proteins, which in turn can be used in a variety of different applications.

The subject proteins also find use in fluorescence activated cell sorting applications. In such applications, the subject fluorescent protein is used as a label to mark a population of cells and the resulting labeled population of cells is then sorted with a fluorescent activated cell sorting device, as is known in the art. FACS methods are described in U.S. Patent Nos. 5,968,738 and 5,804,387; the disclosures of which are herein incorporated by reference.

The subject proteins also find use as in vivo marker in animals (e.g., transgenic animals). For example, expression of the subject protein can be driven by tissue specific promoters, where such methods find use in research for gene therapy, e.g., testing efficiency of transgenic expression, among other applications. A representative application of fluorescent proteins in transgenic animals that illustrates this class of applications of the subject proteins is found in WO 00/02997, the disclosure of which is herein incorporated by reference.

Additional applications of the subject proteins include: as markers following injection into cells or animals and in calibration for quantitative measurements (fluorescence and protein); as markers or reporters in oxygen biosensor devices for monitoring cell viability; as markers or labels for animals, pets, toys, food, etc.; and the like.

The subject fluorescent proteins also find use in protease cleavage assays. For example, cleavage inactivated fluorescence assays can be developed using the subject proteins, where the subject proteins are engineered to include a protease specific cleavage sequence without destroying the fluorescent character of the protein. Upon cleavage of the fluorescent protein by an activated protease fluorescence would sharply decrease due to the destruction of a functional chromophor. Alternatively, cleavage activated fluorescence can be developed using the subject proteins, where the subject proteins are engineered to contain an additional spacer sequence in close proximity/or inside the chromophor. This variant would be significantly decreased in its fluorescent activity, because parts of the functional chromophor would be divided by the spacer. The spacer would be framed by two identical protease specific cleavage sites. Upon cleavage via the activated protease the spacer would be cut out and the two residual "subunits" of the fluorescent protein would be able to reassemble to generate a functional fluorescent protein. Both of the above types of application could be developed in assays for a variety of different types of proteases, e.g., caspases, etc.

The subject proteins can also be used in assays to determine the phospholipid composition in biological membranes. For example, fusion proteins of the subject proteins (or any other kind of covalent or non-covalent modification of the subject proteins) that allows binding to specific phospholipids to
5 localize/visualize patterns of phospholipid distribution in biological membranes also allowing colocalization of membrane proteins in specific phospholipid rafts can be accomplished with the subject proteins. For example, the PH domain of GRP1 has a high affinity to phosphatidyl-inositol tri-phosphate (PIP3) but not to PIP2. As such, a fusion protein between the PH domain of GRP1 and the subject
10 proteins can be constructed to specifically label PIP3 rich areas in biological membranes.

Yet another application of the subject proteins is as a fluorescent timer, in which the switch of one fluorescent color to another (e.g. green to red) concomitant with the ageing of the fluorescent protein is used to determine the
15 activation/deactivation of gene expression, e.g., developmental gene expression, cell cycle dependent gene expression, circadian rhythm specific gene expression, and the like.

The antibodies of the subject invention, described above, also find use in a number of applications, including the differentiation of the subject proteins from
20 other fluorescent proteins.

KITS

Also provided by the subject invention are kits for use in practicing one or
25 more of the above described applications, where the subject kits typically include elements for making the subject proteins, e.g., a construct comprising a vector that includes a coding region for the subject protein. The subject kit components are typically present in a suitable storage medium, e.g., buffered solution, typically in a suitable container. Also present in the subject kits may be antibodies to the
30 provided protein. In certain embodiments, the kit comprises a plurality of different vectors each encoding the subject protein, where the vectors are designed for expression in different environments and/or under different conditions, e.g., constitutive expression where the vector includes a strong promoter for expression

in mammalian cells, a promoterless vector with a multiple cloning site for custom insertion of a promoter and tailored expression, etc.

In addition to the above components, the subject kits will further include instructions for practicing the subject methods. These instructions may be present in the subject kits in a variety of forms, one or more of which may be present in the kit. One form in which these instructions may be present is as printed information on a suitable medium or substrate, e.g., a piece or pieces of paper on which the information is printed, in the packaging of the kit, in a package insert, etc. Yet another means would be a computer readable medium, e.g., diskette, CD, etc., on which the information has been recorded. Yet another means that may be present is a website address which may be used via the internet to access the information at a removed site. Any convenient means may be present in the kits.

The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

I. Introduction

In the following experimental section, we present eleven new GFP-like proteins.

II. Materials and Methods

A. Collection of samples

Samples (100-500 mg of tissue) of *Montastraea cavernosa*, *Condylactis gigantea*, *Scolymia cubensis* and *Ricordea florida* were collected at Florida Keys

Marine Sanctuary (Long Key), under National Marine Sanctuary authorization FKNMS-2000-009. The samples were collected during night dives, candidate specimens were picked on the basis of their appearance under ultraviolet flashlight. Other samples (*Dendronephthya* sp., *Heteractis crispa*, *Discosoma* sp.3, 5 *Zoanthus* sp. 2) were picked from private seawater aquariums.

B. Cloning and expression of GFP-like proteins

Total RNA was isolated from the tissue samples following the protocol described in Chomczynski, P. & Sacchi, N. (1987) *Anal Biochem* **162**, 156-9. Total 10 cDNA was amplified using SMART™ cDNA amplification kit (Clontech). These amplified cDNA samples were used to amplify 3'-fragments of cDNAs coding for GFP-like proteins and then obtain the missing 5'-flanks, exactly as described in Matz, M. V., Fradkov, A. F., Labas, Y. A., Savitsky, A. P., Zaraisky, A. G., Markelov, M. L. & Lukyanov, S. A. (1999) *Nat Biotechnol* **17**, 969-73.. After 15 determining the complete cDNA sequence, the coding regions were amplified using the same cDNA samples as were used to clone the 3'- and 5'-flanks as templates. An upstream ("N-terminal") primer had a 5'-heel (5'-
t**TGA**t**TGA**t**TGA**AGGAGAAatc) carrying stop codons (bold) in all frames and bacterial ribosome-binding site (underlined), followed by the target cDNA 20 sequence (20-22 bases) starting with initiation codon of the ORF. The downstream ("C-terminal") primer was 22-25 bases long and corresponded to the antisense sequence of cDNA around the stop codon of the ORF. The resulting fragments were cloned using pGEM-T vector cloning kit (Promega) following the manufacturer's protocol, using *Escherichia coli* JM109 strain as host. The colonies 25 were grown on LB/agar/carbenicillin plates supplemented with 0.3 mM IPTG for 16-20 hours at 37°C, and then incubated for two days at 4°C. The fluorescent colonies were selected using fluorescent microscope and streaked widely on new plates. The same colonies were used for overnight culture inoculation followed by plasmid isolation and sequencing, to confirm the identity of the clone. The bacteria 30 were harvested from the plates, suspended in 1 ml of PBS and disrupted by sonication. The lysate was cleared by centrifugation, and its fluorescent properties were determined using LS-50B spectrofluorometer (Perkin Elmer Instruments). For

mcavRFP and rfloGFP, the “early” samples were harvested after 24 hours at 37°C, “late” samples – after 24 hours at 37C followed by four days at 4°C.

C. Phylogenetic analysis

5 The alignment of GFP-like proteins (see supplemental data) was constructed after Matz, M. V., Fradkov, A. F., Labas, Y. A., Savitsky, A. P., Zarausky, A. G., Markelov, M. L. & Lukyanov, S. A. (1999) *Nat Biotechnol* **17**, 969-73 taking in account constraints of the protein structure. Then the DNA alignment was made following the protein alignment; excluding the poorly aligned N- and C-
10 terminal regions. The phylogenetic tree was constructed using Tree-Puzzle software (Strimmer, K. & von Haeseler, A. (1996) *Mol. Biol. Evol.* **13**, 964-969) under HKY model of DNA evolution (Hasegawa, M., Kishino, H. & Yano, K. (1985) *J. Mol. Evol.* **22**, 160-174), assuming that the variability of sites follows gamma-distribution with alpha parameter estimated from the dataset. The tree was
15 confirmed to be the maximum likelihood tree by PAML software (Yang, Z. (2000) (University College (http://abacus.gene.ucl.ac.uk/software/paml.html), London, England)) under REV model (Yang, Z. H., Goldman, N. & Friday, A. (1994) *Molecular Biology and Evolution* **11**, 316-324). The tree built by Tree-Puzzle from protein alignment (JTT model, (Jones, D. T., Taylor, W. R. & Thornton, J. M.
20 (1992) *CABIOS* **8**, 275-282) had the same topology but lower support values due to smaller number of informative sites in the protein alignment.

III. Results and Discussion

25 A. Nomenclature

For the sake of clarity of phylogenetic analysis representation, in this paper we are using new nomenclature for GFP-like proteins. Our protein identification tags include four-letter leader composed of first letter of genus name and three initial letters of species name, followed by definition of color type: GFP – green,
30 RFP – red, YFP – yellow, CP – chromoprotein (non-fluorescent). When the species is not defined, the leader is four initial letters of the genus name. In the case of multiple non-identified species of the same genus, a number is added to the leader (such as in dis3GFP or zoan2RFP); in the case of several proteins of

the same color type found in the same species, the number is added to the color definition (such as in scubGFP1 and scubGFP2). For *Aequorea victoria* GFP and drFP583 from *Discosoma sp.*, widely accepted common names are kept: GFP and DsRed.

5

B. New GFP-like proteins

A total of fourteen new GFP-like proteins were cloned and spectroscopically characterized. The spectral features of 11 of these proteins are summarized in Table 1 appearing in the figures, as well as the other figures of the application

10

This subset of 11 includes representatives exhibiting features not seen before in Anthozoan GFP-like proteins. Two green proteins from *Condylactis gigantea* (cgigGFP) and *Heteractis crispa* (hcrlGFP) possess double-peaked excitation spectra very similar to the one of wild-type GFP, suggesting that their chromophores undergo photoconversion between neutral and ionized states (Brejc, K., Sixma, T. K., Kitts, P. A., Kain, S. R., Tsien, R. Y., Ormo, M. & Remington, S. J. (1997) *Proc Natl Acad Sci U S A* **94**, 2306-11; Palm, G. J., Zdanov, A., Gaitanaris, G. A., Stauber, R., Pavlakis, G. N. & Wlodawer, A. (1997) *Nat Struct Biol* **4**, 361-5). The red-emitting protein zoan2RFP, although being very similar to DsRed in the shape of excitation/emission curves, behaves like "timer": it turns green at first and then matures into red (Fig. 1, A and B), similarly to one of the mutant variants of DsRed (Tersikh, A., Fradkov, A., Ermakova, G., Zarsky, A., Tan, P., Kajava, A. V., Zhao, X., Lukyanov, S., Matz, M., Kim, S., Weissman, I. & Siebert, P. (2000) *Science* **290**, 1585-8.). The two new red-emitters from great star coral *Montastraea cavernosa* (mcavRFP) and florida corallimorph *Ricordea florida* (rfloRFP) also show a "timer" phenotype (Fig. 1, C-F). In contrast to zoan2RFP, they failed to mature completely into red in our bacterial expression trials, which resulted in two-peak emission spectra such as shown in Figure 1 (D and F). Remarkably, for both these proteins, the red emission band in the more mature form had major excitation peak virtually identical to the one of the immature green form, the yellow-orange excitation peak being significantly smaller (Fig. 2). This is strikingly different from the rest of the orange-red proteins, in which the red emission is excited best in yellow-orange region (Figure 4, Table 1, spectra E). This unusual shape of excitation spectra may be due to photoconversion of the

30

ionization states of the chromophore (by analogy with green proteins), or to even more profound differences in the chromophore structure. In favor of the latter speaks the fact that the shape of the red emission peaks of mcavRFP and rfpRFP is notably different from other orange-red proteins: it is much narrower and almost symmetrical in contrast to the wide and skewed emission peak of the others (compare spectra E and F in Table 1, Figure 4). Meanwhile, in GFP from *Aequorea victoria*, presence or absence of photoconversion does not have much effect on the shape of emission spectra (Heim, R., Cubitt, A. B. & Tsien, R. Y. (1995) *Nature* **373**, 663-4). The striking similarity of major excitation peaks for mature and immature proteins makes it tempting to suggest that in mcavRFP and rfpRFP, the "built-in" fluorescence resonance energy transfer (FRET) from immature green form of the protein to the mature red form is the major mechanism giving rise to red emission.

C. Structural/spectral types of GFP-like proteins

In our view, the best way to classify GFP-like proteins is by their color as it appears to human eye. We discriminate four color types of GFP-like proteins: green, yellow, orange-red and purple-blue, or chromoproteins (Table 1, Figure 14). All of them share the same fold of polypeptide chain, termed "beta-can" (Ormo, M., Cubitt, A. B., Kallio, K., Gross, L. A., Tsien, R. Y. & Remington, S. J. (1996) *Science* **273**, 1392-5.; Yang, F., Moss, L. G. & Phillips, G. N., Jr. (1996) *Nat Biotechnol* **14**, 1246-51). However, there are substantial differences between these color types as far as the chromophore structure is concerned (see Table 1). In GFP (green color), the chromophore is formed by residues 65-67 (Ser-Tyr-Gly) as a result of condensation between the carbonyl carbon of Ser-65 and the amino nitrogen of Gly-67 that produces a five-member ring, followed by the dehydrogenation of the Tyr-66 methylene bridge. All the green proteins apparently possess the same chromophore, and the differences in the spectral shapes are explained by modifications of its environment. It must be noted that the green proteins having excitation/emission spectra such as on panel A on Table 1 are sometimes called cyan or even blue, but to the human eye the color of these proteins after purification still appears bright green. In the red protein DsRed, the chromophore synthesis includes one more stage that extends the conjugated pi-

system of the chromophore – dehydrogenation of the bond between the alpha carbon and amino nitrogen of the first chromophore-forming residue. Meanwhile, in the chromoproteins representative asulCP, cyclization leads to the formation of a six-member rather than five-member ring, and the critical step in creating the extended conjugated pi-system is breakage of the polypeptide chain immediately before the chromophore. Notably, no other chromoprotein contains such a chain break, as demonstrated by denaturing electrophoresis of the bacterial expression products (data not shown). This indicates that the chromophore structure of asulCP is exception rather than the rule within this color type. Biochemical and mutagenesis studies of the yellow zoanYFP indicated that this protein has yet another chromophore structure. So, it must be concluded that although pronounced color difference between GFP-like proteins indicates difference in chromophore structures (which makes it reasonable to use color for classification), different chromophores might be found even in the proteins of the same color, as it happens within the group of chromoproteins and probably within the orange-red group.

D. Molecular basis of color conversion

Since a chromophore synthesis pathway in DsRed is an extended form of the GFP pathway, it can be easily imagined that any mutation damaging the additional autocatalytic stage in DsRed would convert it into green protein. Indeed, at least seven different mutant variants of DsRed emitting in the green range were found during random and site specific mutagenesis. Similar reasoning should apply to the two new red proteins, because their red emission also arises as a result of further modification of the green-emitting chromophore.

It has been shown that a single amino acid replacement can convert a chromoprotein into a DsRed-like red fluorescent protein. It is particularly unexpected for asulCP from *Anemonia sulcata*, which has been directly demonstrated to contain a very dissimilar chromophore; and it still seems unlikely that its red fluorescent mutant variant actually switches to synthesizing a DsRed-type chromophore instead of original one. However, random mutations in this mutant variant resulted in appearance of green-emitting forms. Since no green-emitting intermediate stage was present in the original asulCP autocatalytic pathway, formation of green-emitting structure in these mutants signifies a

substantial deviation, most probably towards a GFP/DsRed type of chromophore formation sequence judging by the shape of excitation/emission spectra of the green asulCP mutants.

5 Finally, yellow protein zoanYFP also can be converted into green-emitting state by at least two different amino acid replacements.

Taking these data into account, the following explanation of the observed phylogenetic pattern seems plausible: that different chromophore structures, even the most dissimilar ones, are alternative products synthesized with the help of a basically similar autocatalytic environment, rather than outcomes of prolonged
10 evolution of different catalytic mechanisms. Apparently, just a few amino acid changes in the protein may act like a switch between alternative pathways, as exemplified by mutagenesis results on asulCP chromoprotein.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application
15 were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way
20 of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

1. A nucleic acid having a sequence of residues that is substantially the same as or identical to a nucleotide sequence of at least 10 residues in length of SEQ ID NOS:01, 03, 05, 07, 09, 11, 13, 15, 17, 19, 21, 23, 25 or 27.
- 5 2. The nucleic acid according to Claim 1, wherein said nucleic acid has a sequence similarity of at least about 60% with a sequence of at least 10 residues in length of SEQ ID NOS: 01, 03, 05, 07, 09, 11, 13, 15, 17, 19, 21, 23, 25 or 27.
- 10 3. A nucleic acid present in other than its natural environment that encodes a chromo and/or fluorescent protein that has an amino acid sequence of: SEQ ID NOS: 02, 04, 06, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26 or 28.
- 15 4. A nucleic acid that encodes a mutant protein of a protein that has an amino acid sequence of: SEQ ID NOS: 02, 04, 06, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26 or 28.
- 20 5. The nucleic acid according to Claim 4, wherein said mutant protein comprises at least one point mutation as compared to its wild type protein.
6. The nucleic acid according to Claim 4, wherein said mutant protein comprises at least one deletion mutation as compared to its wild type protein.
- 25 7. A fragment of the nucleic acid selected of Claims 1 to 6.
8. An isolated nucleic acid or mimetic thereof that hybridizes under stringent conditions to a nucleic acid of Claims 1 to 7.
9. A construct comprising a vector and a nucleic acid of Claims 1 to 8.
- 30 10. An expression cassette comprising:
 - (a) a transcriptional initiation region functional in an expression host;
 - (b) a nucleic acid selected from the group consisting of the nucleic acids of Claims 1 to 9; and

(c) and a transcriptional termination region functional in said expression host.

11. A cell, or the progeny thereof, comprising an expression cassette according to Claim 10 as part of an extrachromosomal element or integrated into the genome of a host cell as a result of introduction of said expression cassette into said host cell.

12. A method of producing a chromo and/or fluorescent protein, said method comprising:
growing a cell according to Claim 11, whereby said protein is expressed;
and
isolating said protein substantially free of other proteins.

13. A protein or fragment thereof encoded by a nucleic acid selected from the group consisting of Claims 1 to 10.

14. An antibody binding specifically to a protein according to Claim 13.

15. A transgenic cell or the progeny thereof comprising a transgene selected from the group consisting of a nucleic acids according to any of Claims 1 to 10.

16. A transgenic organism capable comprising a transgene selected from the group consisting of a nucleic acids according to any of Claims 1 to 10.

17. In an application that employs a chromo- or fluorescent protein, the improvement comprising:
employing a protein according to Claim 13.

18. In an application that employs a nucleic acid encoding a chromo- or fluorescent protein, the improvement comprising:
employing a nucleic acid according to Claims 1 to 10.

19. A kit comprising a nucleic acid according to Claims 1 to 10 and instructions for using said nucleic acid.

Figure 1.

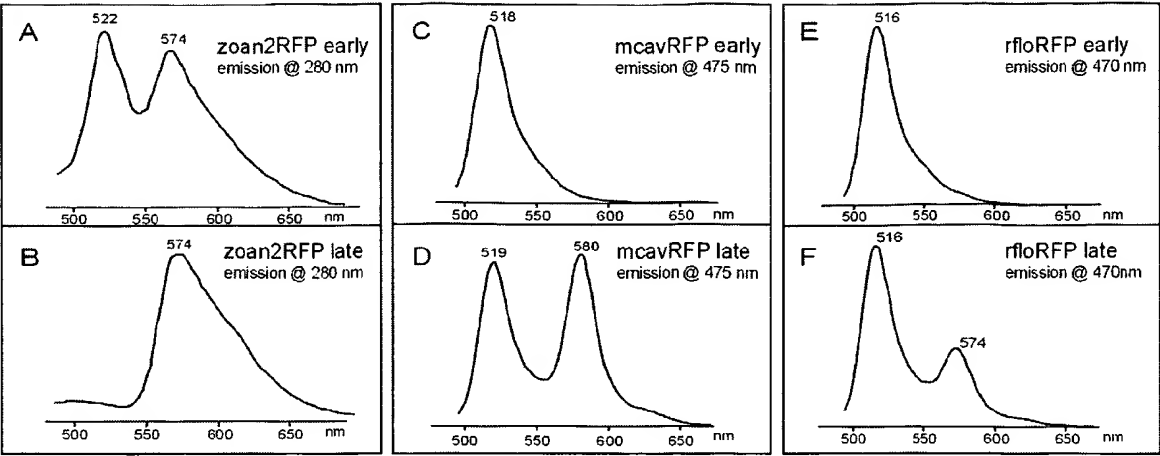


Figure 2.

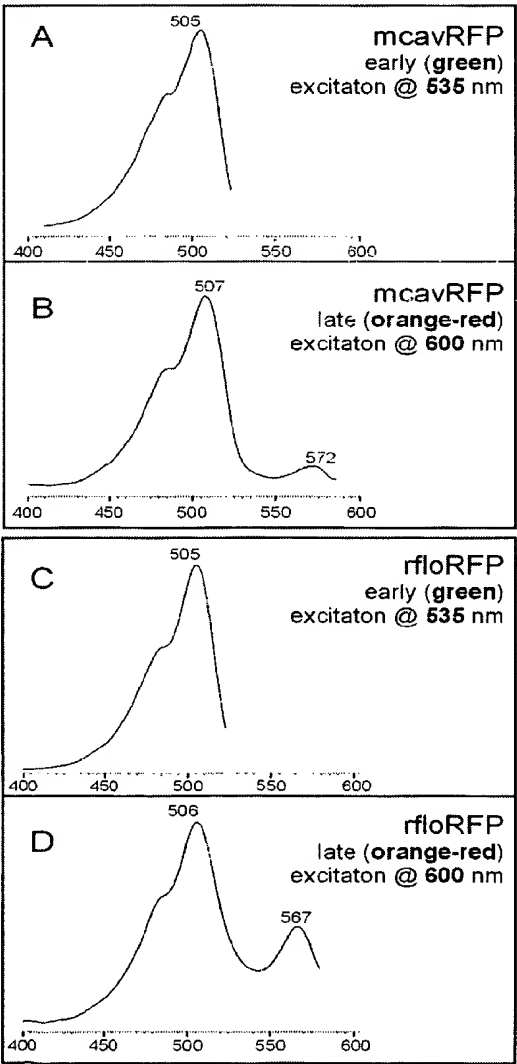


Figure 3.

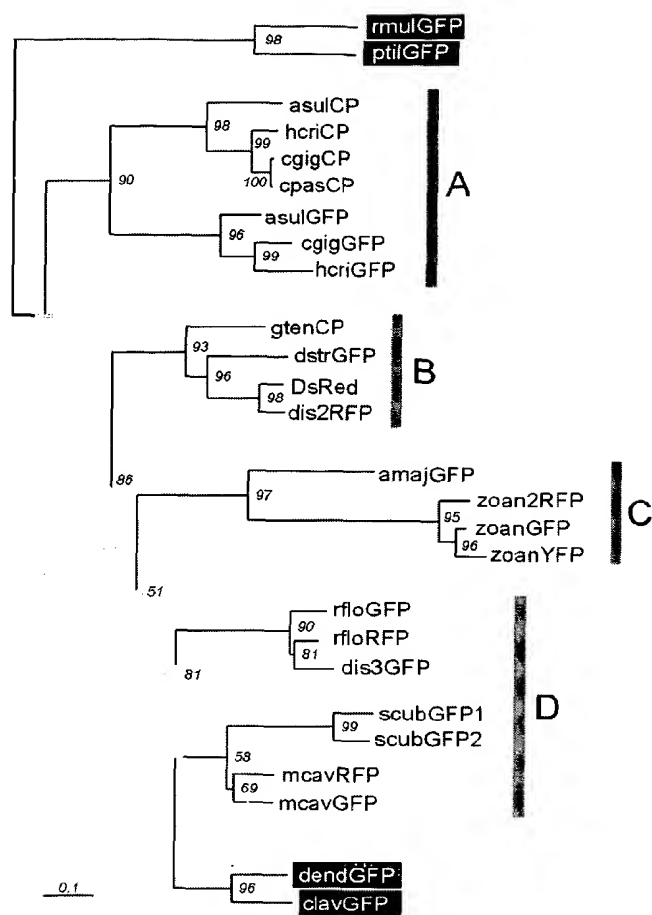


Figure 4

Protein ID (original ID)	GenBank accession #	Reference	Taxonomy Genus species (Class, Sub-class, Order)	Excitation maxima, nm	Emission maxima, nm	Representative spectra excitation emission	Color	Representative chromophore structure
anajGFP (anFP486) dtrGFP (dsFP483) clavGFP (dsFP484)	AF168421 AF168420 AF168424	2 2 2	<i>Anemonia majano</i> (Anthozoa, Zoantharia, Actiniaria) <i>Discosoma striata</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Clavularia</i> sp. (Anthozoa, Aleyonaria, Aleyonacea)	458 456 443	486 484 483		GREEN	
GFP cgigGFP hcrGFP	M62653 AY037776 AF420592	34 this paper this paper	<i>Aequorea victoria</i> (Hydrozoa, ... Hydroida) <i>Condylactis gigantea</i> (Anthozoa, Zoantharia, Actiniaria) <i>Heteractis crispata</i> (Anthozoa, Zoantharia, Actiniaria)	395, 471 399, 482 405, 481	508 496 499			
pluGFP rmuGFP zoanGFP (zFP506) asuGFP (asFP499) disGFP dendGFP mcavGFP rfoGFP scubGFP 1 scubGFP 2	AY015995 AY015996 AF168422 AF322221 AF420593 AF420591 AY037769 AY037772 AY037767 AY037771	35 35 2 4 this paper this paper this paper this paper this paper this paper	<i>Philosaurus</i> sp. (Anthozoa, Aleyonaria, Pennatulacea) <i>Renilla muelleri</i> (Anthozoa, Aleyonaria, Pennatulacea) <i>Zoanthus</i> sp. (Anthozoa, Zoantharia, Zoanthidea) <i>Anemonia sulcata</i> (Anthozoa, Zoantharia, Actiniaria) <i>Discosoma</i> sp. 3 (Anthozoa, Zoantharia, Corallimorpharia) <i>Dendronephthya</i> sp. (Anthozoa, Aleyonaria, Aleyonacea) <i>Montastraea cavernosa</i> (Anthozoa, Zoantharia, Scleractinia) <i>Ricordia florida</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Scolymia cubensis</i> (Anthozoa, Zoantharia, Scleractinia) <i>Scolymia cubensis</i> (Anthozoa, Zoantharia, Scleractinia)	500 498 496 403, 480 499 503 494 506 508 517 497 497	508 510 506 499 512 508 515 517 506 506			
zoanYFP (zFP538)	AF168423	2	<i>Zoanthus</i> sp. (Anthozoa, Zoantharia, Zoanthidea)	494, 528	538		YELLOW	?
DsRed (dFP583) dis2RFP (dsFP593) zoan2RFP	AF168419 AF272711 AY056642	2 36 this paper	<i>Discosoma</i> sp. 1 (Anthozoa, Zoantharia, Corallimorpharia) <i>Discosoma</i> sp. 2 (Anthozoa, Zoantharia, Corallimorpharia) <i>Zoanthus</i> sp. 2 (Anthozoa, Zoantharia, Zoanthidea)	558 573 563	583 593 574		ORANGE-RED	
mcavRFP rfoRFP	AY037770 AY037773	this paper this paper	<i>Montastraea cavernosa</i> (Anthozoa, Zoantharia, Scleractinia) <i>Ricordia florida</i> (Anthozoa, Zoantharia, Corallimorpharia)	507, 572 506, 567	519, 580 516, 574		?	?
asuICP (asCP)	AF246709	3, 4	<i>Anemonia sulcata</i> (Anthozoa, Zoantharia, Actiniaria)	568	none		PURPLE-BLUE	
hcrICP (hcCP) cgigCP (cgCP) cpasCP (cpCP) glenCP (glCP)	AF363776 AF363775 AF383155 AF383156	5 5 5 5	<i>Heteractis crispata</i> (Anthozoa, Zoantharia, Actiniaria) <i>Condylactis gigantea</i> (Anthozoa, Zoantharia, Actiniaria) <i>Condylactis passiflora</i> (Anthozoa, Zoantharia, Actiniaria) <i>Goniopora tenuidens</i> (Anthozoa, Zoantharia, Scleractinia)	578 571 571 580	none none none none		?	?

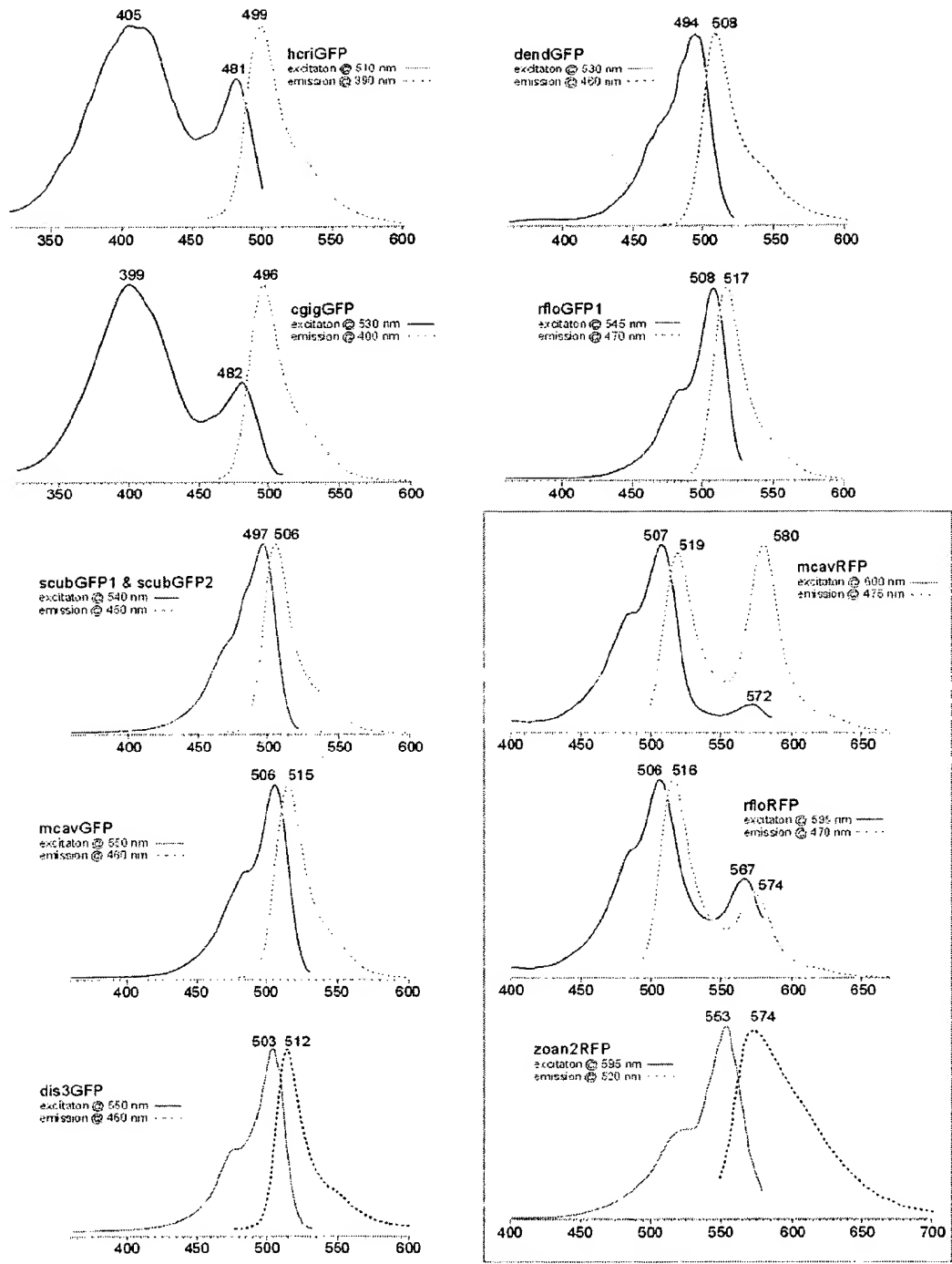
Table 1. Summary of spectral features and chromophore structures in the family of GFP-like proteins. Note that this paper uses different names for GFP-like proteins than proposed in original publications (the original names, where available, are given in brackets in the first column; see text for nomenclature details).

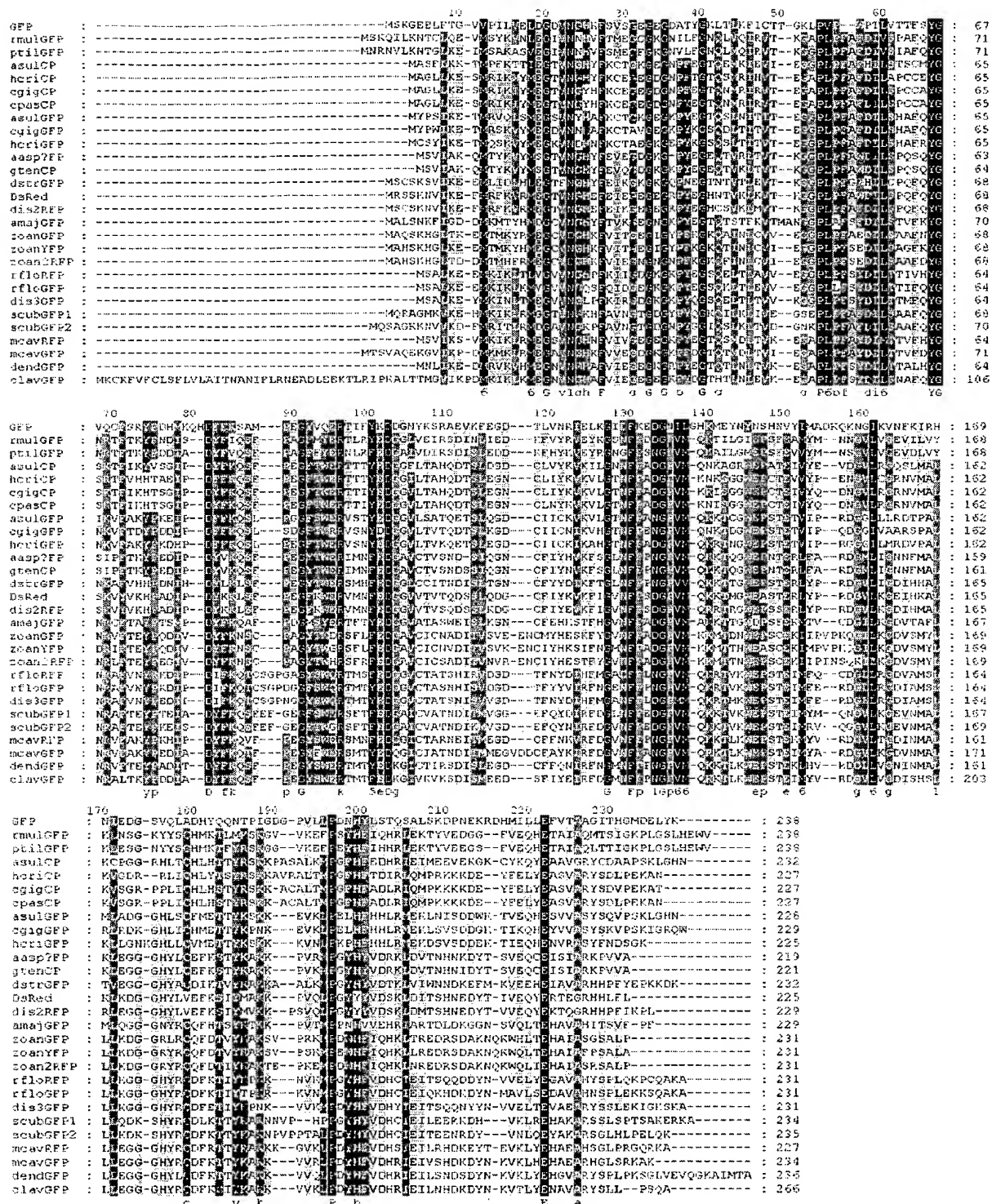
Figure 5

Table 2

clade	colors	Zoantharia orders
A	Green, purple-blue	Actiniaria
B	Green, orange-red, purple-blue	Corallimorpharia, Scleractinia
C	Green, yellow, orange-red	Actiniaria, Zoanthidea
D	Green, orange-red	Corallimorpharia, Scleractinia

Figure 6





Green fluorescent protein from *Heteractis crispa* hcriGFP

10	20	30	40	50	60
ATTTTGGACAGGTGTTCAACCAAGCAAATTTAAGAAGTCATCATCTTTATCTCAGTCAGG					
70	80	90	100	110	120
AAAATGTGTTCTTACATCAAAGAAACCATGCAAAGTAAGGTTTACATGGAAGGAAAAGTT					
M	C	S	Y	I	K
E	T	M	Q	S	K
V	Y	M	E	G	K
V					
130	140	150	160	170	180
AACGACCACAACCTTCAAGTGCACCTGCAGAAGGAAAAGGAGAACCATACAAAGGCTCACAA					
N	D	H	N	F	K
C	T	A	E	G	K
G	E	P	Y	K	G
S	Q				
190	200	210	220	230	240
AGCCTGACGATCACCGTAACTGAAGGAGGTCTCTGCCATTTCGCTTCGACATTCTTTCA					
S	L	T	I	T	V
T	E	G	G	P	L
P	F	A	F	D	I
L	S				
250	260	270	280	290	300
CACGCCTTTTCGATATGGCAATAAGGTGTTTCGCCAAGTACCCCAAAGATCATCCTGATTTT					
H	A	F	R	Y	G
N	K	V	F	A	K
Y	P	K	D	H	P
D	F				
310	320	330	340	350	360
TTTAAGCAGTCTCTTCTCTGAAGGTTTTACTTGGGAAAAGAGTAAGCAACTATGAGGACGGA					
F	K	Q	S	L	P
E	G	F	T	W	E
R	V	S	N	Y	E
D	G				
370	380	390	400	410	420
GGAGTCCTTACCGTTAAACAAGAACTAGTCTGGAGGGAGATTGCATTATTTGCAAATTT					
G	V	L	T	V	K
Q	E	T	S	L	E
G	D	C	I	I	C
K	I				
430	440	450	460	470	480
AAAGCACATGGCACTAAGTTCCTCCCGCAGATGGTCCGGTGATGCAAAAACGGACCAATGGA					
K	A	H	G	T	N
F	P	A	D	G	P
V	M	Q	K	R	T
N	G				
490	500	510	520	530	540
TGGGAGCCATCAACTGAAACGGTTATTCCACGGGGTGGAGGAATTCTGATGCGCGATGTG					
W	E	P	S	T	E
T	V	I	P	R	G
G	G	G	I	L	M
R	D	V			
550	560	570	580	590	600
CCCGCACTGAAGCTGCTTGGTAACAAAGGACATCTTCTCTGCGTCATGGAAACAACCTTAC					
P	A	L	K	L	L
G	N	K	G	H	L
L	C	V	M	E	T
T	Y				
610	620	630	640	650	660
AAGTCAAAAAAAAAAAGGTGAACCTGCCAAACCGCACTTTTCATCATTTGAGAATGGAGAAG					
K	S	K	K	K	G
E	P	A	K	P	H
F	H	H	L	R	M
E	K				
670	680	690	700	710	720
GATAGTGTTAGTGACGATGAGAAGACCATTGAGCAGCACGAGAATGTGAGGGCAAGCTAC					
D	S	V	S	D	D
E	K	T	I	E	Q
H	E	N	V	R	A
S	Y				
730	740	750	760	770	780
TTCAATGATAGTGGAATGATCATTTCCTTATTGATTTCAATGTTAGGGCATTTCAGTTT					
F	N	D	S	G	K
*					
790	800	810	820	830	840
CCAAATTTTCTTAGACACAGTCTTTTCCTTTAGCTTCGTAGCCTACTTACCCATGTTTTG					
850	860				
TTGAAGTCAATAAATAGCTAAGCACTAC (SEQ ID NOS: 01 & 02)					

Figure 9

Green fluorescent protein from *Dendronephthya* sp. dendGFP

```
      10      20      30      40      50      60
5'CATATCGAGAAAGTTGTGAAACCAAATTCTTACTCTACTTTTACTACCATGAATCTGATT
                                     M N L I

      70      80      90     100     110     120
AAAGAAGATATGAGGGTTAAGGTGCATATGGAAGGGAATGTAAACGGGCATGCTTTTGTG
K E D M R V K V H M E G N V N G H A F V

     130     140     150     160     170     180
ATTGAAGGGGAAGGAAAAGGAAGGCCCTACGAAGGGACACAGACCTTGAACCTGACAGTG
I E G E G K G R P Y E G T Q T L N L T V

     190     200     210     220     230     240
AAAGAAGGCGCGCCTCTCCCATTTTCTTACGACATCTTGACAACAGCATTGCACTACGGA
K E G A P L P F S Y D I L T T A L H Y G

     250     260     270     280     290     300
AACAGAGTATTTCACTGAATACCCAGCAGATATCACGGATTATTTCAAGCAATCATTTCTT
N R V F T E Y P A D I T D Y F K Q S F P

     310     320     330     340     350     360
GAAGGATATTCCTGGGAAAGAACCATGACTTATGAAGACAAGGGCATTGTACCATCAGA
E G Y S W E R T M T Y E D K G I C T I R

     370     380     390     400     410     420
AGCGACATAAGCTTGGAAGGTGACTGCTTTTTTCCAAAACATTCGTTTTAATGGGATGAAC
S D I S L E G D C F F Q N I R F N G M N

     430     440     450     460     470     480
TTTCCCCCAAATGGTCCAGTTATGCAGAAGAAAACCTTTGAAGTGGAACCA1CCACAGAG
F P P N G P V M Q K K T L K W E P S T E

     490     500     510     520     530     540
AAGCTGCACGTGCGTGATGGGTTGCTTGTCGGTAATATTAACATGGCTCTGCTGCTTGAA
K L H V R D G L L V G N I N M A L L L E

     550     560     570     580     590     600
GGAGGTGGACATTACCTGTGTGACTTCAAACTACTTACAAAGCGAAGAAGGTTGTTTCAG
G G G H Y L C D F K T T Y K A K K V V Q

     610     620     630     640     650     660
TTGCCAGATTATCATTTTGTGGACCATCGCATTGAGATCTTGAGTAATGACAGCGATTAC
L P D Y H F V D H R I E I L S N D S D Y

     670     680     690     700     710     720
AACAAAGTGAAGCTGTACGAGCATGGGGTTGCTCGCTATTCTCCGTTGCCCAAGTCAGGC
N K V K L Y E H G V A R Y S P L P K S G

     730     740     750     760     770     780
CTGGTAGAGGTTCAAGGGAAAGCCATAATGACTGCATAGATAAACATGTAGTGAAGACCA
L V E V Q G K A I M T A *

     790     800     810     820     830     840
CATACTCGGGATTAGAGTTTAGGGATTGGTAGTTGTGGTAGATTCTAGCCTACAAATTTT
```

TTGGG 3' (SEQ ID NO:03 & 04)

Figure 10

Red fluorescent protein from *Zoanthus* sp. zoanRFP

```

      10      20      30      40      50      60
GAGTTGAGTTCTCGACTTCAGTTGTATCACTTTTGACGTATCAAGTGATCTATCTCAAC

      70      80      90     100     110     120
ATGGCCCATTCAAAGCACGGACTAACAGATGACATGACAATGCATTTCCGTATGGAAGGG
M  A  H  S  K  H  G  L  T  D  D  M  T  M  H  F  R  M  E  G

     130     140     150     160     170     180
TGCGTTCGATGGACATAAGTTTGTAAATCGAGGGCAACGGCAATGGAATCCTTTCAAAGGG
C  V  D  G  H  K  F  V  I  E  G  N  G  N  G  N  P  F  K  G

     190     200     210     220     230     240
AAACAGTTTATTAATCTGTGTGTGATTGAAGGAGGACCACTGCCATTCTCCGAAGACATA
K  Q  F  I  N  L  C  V  I  E  G  G  P  L  P  F  S  E  D  I

     250     260     270     280     290     300
TTGTCTGCTGCGTTTGACTACGGAAACAGGCTCTTCACTGAATATCCTGAAGGCATAGTT
L  S  A  A  F  D  Y  G  N  R  L  F  T  E  Y  P  E  G  I  V

     310     320     330     340     350     360
GACTATTTCAAGAACTCGTGTCTGCTGGATATACGTGGCACAGGTCTTTTCGCTTTGAA
D  Y  F  K  N  S  C  P  A  G  Y  T  W  H  R  S  F  R  F  E

     370     380     390     400     410     420
GATGGAGCAGTTTGCATATGCAGTGCAGATATAACAGTAAATGTTAGGGAAAACCTGCATT
D  G  A  V  C  I  C  S  A  D  I  T  V  N  V  R  E  N  C  I

     430     440     450     460     470     480
TATCATGAGTCCACGTTTATGGAGTGAACCTTTCCTGCTGATGGACCTGTGATGAAAAAG
Y  H  E  S  T  F  Y  G  V  N  F  P  A  D  G  P  V  M  K  K

     490     500     510     520     530     540
ATGACAACTAATTGGGAACCGTCCTGCGAGAAAATCATACCAATAAATAGTCAGAAGATA
M  T  T  N  W  E  P  S  C  E  K  I  I  P  I  N  S  Q  K  I

     550     560     570     580     590     600
TTAAAAGGGGATGTCTCCATGTACCTCCTTCTGAAGGATGGTGGGCGTTACCGCTGCCAG
L  K  G  D  V  S  M  Y  L  L  L  K  D  G  G  R  Y  R  C  Q

     610     620     630     640     650     660
TTTGACACAATTTACAAAGCAAAGACTGAGCCAAAAGAAATGCCGGACTGGCACTTCATC
F  D  T  I  Y  K  A  K  T  E  P  K  E  M  P  D  W  H  F  I

     670     680     690     700     710     720
CAGCATAAGCTCAACCGTGAAGACCGCAGCGATGCTAAGAATCAGAAATGGCAACTGATA
Q  H  K  L  N  R  E  D  R  S  D  A  K  N  Q  K  W  Q  L  I

     730     740     750     760     770     780
GAACATGCTATTGCATCCCGATCTGCTTTACCCCTGATAACAAAGGAGTTGCTATTGCATG
E  H  A  I  A  S  R  S  A  L  P  *

     790     800     810     820     830     840
TGCATGCCTATTACGCTGATAAAAAATGTAGTTTAAACATGCAATTGTATGTGCATGCACA

     850
TTACCCTGATA

```

(SEQ ID NOS:05 & 06)

Figure 11

Green fluorescent protein from *Scolymia cubensis* scubGFP1 (AY037767)

```

      10      20      30      40      50      60
5'TGTGACATTTCAGTCATATAGGAGCCTCTATCGGAGCTGAGGTCCCATTACCGTTGTGAT
      70      80      90     100     110     120
TTGGACGGGAGCAGATCGAGAACAACMAGGGCTGTACGAGTCTGATAATTTACTTTACAT
     130     140     150     160     170     180
CTACCAACATGCAGCGTGCTGGGATGAAGGTTAAGGAACATATGAAGATCAAACGCGTA
      M  Q  R  A  G  M  K  V  K  E  H  M  K  I  K  L  R  M

     190     200     210     220     230     240
TGGGAGGTACTGTAAACGGAAGCATTTTCGCGGTTAATGGGACAGGAGACGGCTACCCTT
      G  G  T  V  N  G  K  H  F  A  V  N  G  T  G  D  G  Y  P  Y

     250     260     270     280     290     300
ATCAGGGAAACAGATTTTGAACCTTATCGTCGAAGGCAGCGAACCTCTGCCTTTTCGCTT
      Q  G  K  Q  I  L  K  L  I  V  E  G  S  E  P  L  P  F  A  F

     310     320     330     340     350     360
TTGATATCTTGTCTCAGCAGCATTCCAGTATGGCAACAGGGCATTACCGAATACCCAACAG
      D  I  L  S  A  A  F  Q  Y  G  N  R  A  F  T  E  Y  P  T  E

     370     380     390     400     410     420
AGATAGCAGACTATTTCAAGCAGTCGTTTGAGTTTGGCGAGGGGTTCTCCTGGGAACGAA
      I  A  D  Y  F  K  Q  S  F  E  F  G  E  G  F  S  W  E  R  S

     430     440     450     460     470     480
GTTTCACITTCGAAGATGGGGCCATTTCGCTCGCCACCAACGATATAACGATGGTTGGTG
      F  T  F  E  D  G  A  I  C  V  A  T  N  D  I  T  M  V  G  G

     490     500     510     520     530     540
GTGAGTTTCAGTATGATATTCGATTGATGGTCTGAACCTCCCTGAAGATGGTCCAGTGA
      E  F  Q  Y  D  I  R  F  D  G  L  N  F  P  E  D  G  P  V  M

     550     560     570     580     590     600
TGCAAAAGAAAACCGTAAAAATGGGAGCCATCCACTGAGATAATGTATATGCAAAATGGAG
      Q  K  K  T  V  K  W  .  E  P  S  T  E  I  M  Y  M  Q  N  G  V

     610     620     630     640     650     660
TGCTGAAGGGTGAGGTTAACATGGCTCTGTGCTTCAAGACAAAAGCCATTACCGTTGCG
      L  K  G  E  V  N  M  A  L  L  L  Q  D  K  S  H  Y  R  C  D

     670     680     690     700     710     720
ACCTCAAAACTACTTTACAAAGCTAAGAATAATGTGCCGCATCCTCCAGGCTACCACTATG
      L  K  T  T  Y  K  A  K  N  N  V  P  H  P  P  G  Y  H  Y  V

     730     740     750     760     770     780
TGGATCACTGCATTGAAATACTCGAAGAACGTAAGGATCACGTTAAGCTGCCGGGAGCATG
      D  H  C  I  E  I  L  E  E  R  K  D  H  V  K  L  R  E  H  A

     790     800     810     820     830     840
CTAAAGCTCGTTCTAGCCTGTACCTACCAGTGCAAAAGAACGAAAGGCTTAGGTGATAG
      K  A  R  S  S  L  S  P  T  S  A  K  E  R  K  A  *

     850     860     870     880     890     900
TCAAAAAGACAACAAGACGAAAATGAAAGGTGTTTCATTGTTAGAATTTGATATTTTCGAT
     910     920     930     940     950     960
TCAATGATTTCGTTAAGGGATTTCGCTAGAGGCTAGCTAACAGGTTAACATCATAAGGATAG
     970     980     990    1000    1010    1020
AGATTTCGTTGCGGAGTTAGAACCTTWTATTTTCCGAATTCAMCTAGAGTCGTTGAGA
    1030    1040    1050    1060    1070    1080
AATTTATTAGAGACTAGCTTTAGAGTTACTTTTGTGGAAAAAAGGTTTCCATTTTGTGC
    1090    1100    1110    1120    1130    1140
GTTATTACAGCATTTAAAGCATAGGAATAGAGATTCGGTTATGGAAAATAACAGTAGGAA
    1150    1160    1170
AATACGTTGTGAAAATAAACTTGTGTGCGAAAAA 3'
```

(SEQ ID NOS:07&08)

FIGURE 12

Green fluorescent protein from *Scolymia cubensis* scubGFP2 (AY037771)

```

      10      20      30      40      50      60
5'CCTGGTGATTTGGACGAGAGCAGATCGAGAATAGCAAGGTTTACCAGCGTGATAATTTA
      70      80      90     100     110     120
CTTTACATCTAACAACATGCAATCTGCTGGGAAGAAGAATGTCGTTAAGGACTTCATGAA
      M Q S A G K K N V V K D F M K

      130     140     150     160     170     180
GATCACACTGCGTATGGACGGTGCTGTAAACGGGAAGCCCTTCGCGGTTAATGGAACAGG
      I T L R M D G A V N G K P F A V N G T G

      190     200     210     220     230     240
AGATGGCAACCCTTATGGTGGAATACAGAGTTTGAAGCTTACCGTCGATGGCAACAAACC
      D G N P Y G G I Q S L K L T V D G N K P

      250     260     270     280     290     300
TCTGCCTTTTGCTTTTGATATCTTGTGAGCAGCATTCAGTATGGCAACAGGGCATTAC
      L P F A F D I L S A A F Q Y G N R A F T

      310     320     330     340     350     360
CGAATACCCAAAAGAGATATCAGACTATTTCAAGCAGTCGTTTGAGTTGGCGAGGGGTT
      E Y P K E I S D Y F K Q S F E F G E G F

      370     380     390     400     410     420
TACCTGGGAACGAAGTTTCACTTTCGAAGACGGGGCCATTTGCGTCGCCACGAACGATAT
      T W E R S F T F E D G A I C V A T N D I

      430     440     450     460     470     480
AAAGATGGTTGGCGATGAGTTTCAATATAACATTTCGATTTGATGGTGTGAATTTCCCTGA
      K M V G D E F Q Y N I R F D G V N F P E

      490     500     510     520     530     540
AGATGGTCCWGTYATGCAGAAGAAAACGGTGAAGTGGGAGCCATCCACAGAGATAATGCG
      D G P V M Q K K T V K W E P S T E I M R

      550     560     570     580     590     600
TGTGCAAGGTGGAGTGCTAAAGGGTGAGGTTAACATGGCTCTGTTGCTTAAAGACAAAAG
      V Q G G V L K G E V N M A L L L K D K S

      610     620     630     640     650     660
CCATTACCGATGTGACTTCAAACTACTTACAAAGCTAAGAATCCTGTCCCGCCGACGGC
      H Y R C D F K T T Y K A K N P V P P T A

      670     680     690     700     710     720
GCTTCCAGACTACCACTATGTGGATCACTGTATTGAAATCACCGAGGAAAATAGGGATTA
      L P D Y H Y V D H C I E I T E E N R D Y

      730     740     750     760     770     780
CGTTAAGCTGCAGGAGTATGCTAAAGCTCGTTCTGGCCTGCACCTGCCCGAACTGCAAAA
      V K L Q E Y A K A R S G L H L P E L Q K

      790     800     810
GTAAAGGCTTAGGCGATAGTCAAGACGACAACGAGAAGA 3'
*
```

(SEQ ID NO:09 & 10)

FIGURE 13

Red fluorescent protein from *Ricordea florida* rflorRFP (AY037773)

```
      10      20      30      40      50      60
5'TGTGAAAGTTAACATTTTACTTTACTTCTACCGCATGAGTGCCTCAAGAGGAAATGA
      M S A L K E E M K

      70      80      90     100     110     120
AAATCAAGCTTACATTGGTGGCGTTGTTAACGGGCACCCATTCAAGATCATTGGGGACG
      I K L T L V G V V N G H P F K I I G D G

      130     140     150     160     170     180
GAAAGGGCAAACCTATGAGGGATCGCAGGAATTAACCTTGCCGTGGTGAAGGAGGGC
      K G K P Y E G S Q E L T L A V V E G G P

      190     200     210     220     230     240
CTCTGCCTTTCTCTTATGATATCCTGACAACGATAGTTCACCTATGGCAACAGGGCATTG
      L P F S Y D I L T T I V H Y G N R A F V

      250     260     270     280     290     300
TGAACTACCCAAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCCTGGTGCTG
      N Y P K D I P D I F K Q T C S G P G A G

      310     320     330     340     350     360
GATATTCCTGGCAAAGGACCATGAGTTTTGAAGACGGAGGCGTTTGCCTGCTACGAGCC
      Y S W Q R T M S F E D G G V C T A T S H

      370     380     390     400     410     420
ATATCAGGGTGGATGGCGACACTTTCATTATGACATTCACCTCATGGGAGCGGATTTCC
      I R V D G D T F N Y D I H F M G A D F P

      430     440     450     460     470     480
CTCTTAATGGTCCAGTGATGCAGAAAAGAACAGTGAAATGGGAGCCATCCACTGAGATAA
      L N G P V M Q K R T V K W E P S T E I M

      490     500     510     520     530     540
TGTTTCAATGTGATGGATGCTGAGGGGTGATGTTGCCATGTCTCTGTTGCTGAAAGGAG
      F Q C D G L L R G D V A M S L L L K G G

      550     560     570     580     590     600
GCGGCATTACCGATGTGACTTTAAAACTATTTATAAACCCCAAGAAGATGTCAAGATGC
      G H Y R C D F K T I Y K P K K N V K M P

      610     620     630     640     650     660
CAGGTTACCATTTTGTGGACCACTGCATTGAGATAACGAGTCAACAGGACGATTACAACG
      G Y H F V D H C I E I T S Q Q D D Y N V

      670     680     690     700     710     720
TGTTTGAGCTGTACGAGGGTGCTGTAGCCCACTACTCTCTCTGCAGAAACCATGCCAAG
      V E L Y E G A V A H Y S P L Q K P C Q A

      730     740     750     760     770     780
CAAAGGCATAAAGCCAAACAACCCAAGAGGACAACAAGACATTTAATCAAATCACATCTT
      K A *

      790     800
TGTATTTTGGTTAGAGTTGAAAAAAA 3'
```

(SEQ ID NO:11 & 12)

FIGURE 14

Green fluorescent protein from *Ricordea florida* rfloGFP (AY037772)

```

      10      20      30      40      50      60
5'AGTCACCTCGGTGTTTTAGGACAGGAAGGATCACGAGCAAGAGAAGAAGTGTGAAAGTT
      70      80      90     100     110     120
AACACTTTACTCTACTTCTACCGCATGAGTGCACTCAAAGAGGAAATGAAAATCAAGCT
              M S A L K E E M K I K L

      130     140     150     160     170     180
TAAATGGTGGGCGTTGTTAACGGGCAGTCATTTAGATCGATGGGGAAGGAAAAGGCAA
      K M V G V V N G Q S F Q I D G E G K G K

      190     200     210     220     230     240
ACCTTACGAGGGATCACAGAAATTAACCCCTGAAGTGGTGGAGGAGGGCTCTGCTCTT
      P Y E G S Q K L T L E V V E G G P L L F

      250     260     270     280     290     300
CTCTTATGATATCCTGACAACGATATTTTCACTATGGCAACAGGGCATTCGTGAACTACCC
      S Y D I L T T I F Q Y G N R A F V N Y P

      310     320     330     340     350     360
AAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCCTGATGGTGGATTTTCCTG
      K D I P D I F K Q T C S G P D G G F S W

      370     380     390     400     410     420
GCAAAGGACCATGACTTATGAAGACGGAGGGGTTTGCACTGCTTCAAACCACATCAGCGT
      Q R T M T Y E D G G V C T A S N H I S V

      430     440     450     460     470     480
GGACGGCGACACTTTTTATTATGTGATAAGATTTAATGGAGAGAATTTTCTCCAAATGG
      D G D T F Y Y V I R F N G E N F P P N G

      490     500     510     520     530     540
TCCAGTAATGCAGAAAAGAACAGTGAAATGGGAGCCATCCACTGAGATAATGTTTGAACG
      P V M Q K R T V K W E P S T E I M F E R

      550     560     570     580     590     600
TGATGGATTGCTGAGGGGTGACATTGCCATGTCTCTGTTGCTGAAAGGAGGCGGCCATTA
      D G L L R G D I A M S L L K G G G H Y

      610     620     630     640     650     660
CCGATGTGACTTTAAACTATTTATACACCCAAGAGGAAGGTCAACATGCCAGGTTACCA
      R C D F K T I Y T P K R K V N M P G Y H

      670     680     690     700     710     720
TTTTGTGGACCACTGCATTGAGATACAGAAGCACGACAAGGATTACAACATGGCTGTGCT
      F V D H C I E I Q K H D K D Y N M A V L

      730     740     750     760     770     780
CTCTGAGGATGCTGTAGCCCACTCTCTCTGGAGAAAAAAGCCAAGCAAAGGCGTA
      S E D A V A H N S P L E K K S Q A K A *

      790
AAGCCAAACAACCTAA 3'
```

(SEQ ID NO:13&14)

Figure 15

Red fluorescent protein from *Montastraea cavernosa* mcavRFP (AY037770)

```
      10      20      30      40      50      60
5'ACGCAGGGATTACCCCTGGTGATTTGGAAGAGAGCAGACCGAGAACAACAAGAGCTGTAT
      70      80      90     100     110     120
AAGGCTGATATCTTACTTTACGTCTACCATCATGAGTGTGATTAATCAGTCATGAAGAT
R L I S Y F T S T I M S V I K S V M K I

      130     140     150     160     170     180
CAAGCTGCGTATGGAAGGCAGTGTAACGGGCACAACCTTCGTAATTGTTGGAGAAGGAGA
K L R M E G S V N G H N F V I V G E G E

      190     200     210     220     230     240
AGGCAAGCCTTATGAGGGAACACAGAGTATGGACCTTACAGTCAAAGAAGGCGCACCTCT
G K P Y E G T Q S M D L T V K E G A P L

      250     260     270     280     290     300
GCCTTTGCGCTACGATATCATGACAACAGTATTCCATTACGGCAATAGGGTATTCGCAA
P F A Y D I M T T V F H Y G N R V F A K

      310     320     330     340     350     360
ATACCCAAACATATCCCAGACTATTTCAAGCAGATGTTTCCTGAGGAGTATTCCTGGGA
Y P K H I P D Y F K Q M F P E E Y S W E

      370     380     390     400     410     420
ACGAAGCATGAATTTGGAAGGCGGGGCATTTCACCGCCAGGAACGAGATAACAATGGA
R S M N F E G G G I C T A R N E I T M E

      430     440     450     460     470     480
AGGCGACTGTTTTTCAATAAAGTTGATTTGATGGTGTGAACCTTCCCCCAATGGTCC
G D C F F N K V R F D G V N F P P N G P

      490     500     510     520     530     540
AGTCATGCAGAAGAAGACGCTGAAATCGGAGCCATCCACTGAAAAAATGTATGTGCGTGA
V M Q K K T L K W E F S T E K M Y V R D

      550     560     570     580     590     600
TGGAGTGCTGACGGGTGATATCAACATGGCTTTGTTGCTTGAAGGAGGTGGCCATTACCG
G V L T G D I N M A L L L E G G G H Y R

      610     620     630     640     650     660
ATGTGACTTCAGAACTACTTACAGAGCTAAGAAGAAGGGTGTCAAGTTACCAGATTATCA
C D F R T T Y R A K K K G V K L P D Y H

      670     680     690     700     710     720
CTTTGAGGATCACTCCATTGAGATTTTGGCCATGACAAAGAATACTGAGGTAAAGCT
F E D H S I E I L R H D K E Y T E V K L

      730     740     750     760     770     780
GTATGAGCATGCCGAAGCTATTCTGGGCTGCCGAGGGTGGCAAAGTAAAGGCTTAACGA
Y E H A E A H S G L P R V A K *

      790
AAAGCCAAGACCACA 3'
```

(SEQ ID NO:15 & 16)

FIGURE 16

Green fluorescent protein from *Montastraea cavernosa* mcavGFP (AY037769)

```

      10      20      30      40      50      60
5'ATTCCGCGCTGGTGATTGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTAAGGTTGATA
      70      80      90     100     110     120
TCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAACCAG
      M T S V A Q E K G V I K P D

      130     140     150     160     170     180
ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAACGGGCACAAGTTCGTGGTTGAAG
      M K M K L R M E G A V N G H K F V V E G

      190     200     210     220     230     240
GAGATGGAAAAGGGAAGCCTTTTCGACGGAACACAGACTATGGACCTTACAGTCATAGAAG
      D G K G K P F D G T Q T M D L T V I E G

      250     260     270     280     290     300
GCGCACCATTTGCCTTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG
      A P L P F A Y D I L T T V F D Y G N R V

      310     320     330     340     350     360
TATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGT
      F A K Y P E D I A D Y F K Q T F P E G Y

      370     380     390     400     410     420
ACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTTCATCGCCACAACGACA
      F W E R S M T Y E D Q G I C I A T N D I

      430     440     450     460     470     480
TAACAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTGATGGTGTGA
      T M M E G V D D C F A Y K I R F D G V N

      490     500     510     520     530     540
ACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCCATCCACTG
      F P A N G P V M Q R K T L K W E P S T E

      550     560     570     580     590     600
AGATAATGTATGCGCCTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTG
      I M Y A R L G V L K G D V N M A L L L E

      610     620     630     640     650     660
AAGGAGGTGGCCATTACCGATGTGACTTCAAACTACTTACAAAGCTAAGAAGGTTGTCC
      G G G H Y R C D F K T T Y K A K K V V R

      670     680     690     700     710     720
GGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATTGTGAGCCACGACAAAGATT
      L P D Y H F V D H R I E I V S H D K D Y

      730     740     750     760     770     780
ACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAAGGAAGGCCA
      N K V K L H E H A E A R H G L S R K A K

      790     800     810     820     830     840
AGTAAAGGCTTAATGAAAAGTCAAGACGACAACGAGGAGAAACAAAGTACTTTTTTGTTA
      *

      850     860     870     880     890     900
AATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTGTTCGG
      910     920     930     940     950     960
GGATTGTGTTAGAGACTAGCTCTAGAGTTGTATTTGTGAAAAAAGATAGTTTCCAGTTT
      970     980     990     1000    1010    1020
TGCGGGATTACAGCATGGGGATAGACTTTTTAACTCAGTTGTGGTCAAATGCAAGTAAG
      1030    1040    1050    1060
AAAACGTAGTGAGAATAAACTTGTTATCGAAGCCGAAAAAAAAA 3'

```

(SEQ ID NOS: 17 & 18)

Figure 17

Green fluorescent protein from *Condylactis gigantea* cgigGFP (AY037776)

```

      10      20      30      40      50      60
5'ACAGCTGTTTCATCCACGCTCATTCAAGACGCCGTCAACTTTATTCCAGTCAGGAAAATGT
                                     M Y

      70      80      90     100     110     120
ATCCTTGGATCAAGGAAACCATGCGCAGTAAGGTTTACATGGAAGGAGATGTTAACAACC
P W I K E T M R S K V Y M E G D V N N H

     130     140     150     160     170     180
ACGCCTTCAAGTGCAGTGCAGTAGGAGAAGGAAAACCATACAAAGGCTCACAAGACCTGA
A F K C T A V G E G K P Y K G S Q D L T

     190     200     210     220     230     240
CGATTACCGTCACTGAAGGAGTCTCTGCCATTTGCTTTTCGACATTCTTTCACACGCCT
I T V T E G G P L P F A F D I L S H A F

     250     260     270     280     290     300
TTCAGTATGGCAACAAGGTGTTACCGATTACCCGACGATATTCCTGATTTCTTTAAGC
Q Y G N K V F T D Y P D D I P D F F K Q

     310     320     330     340     350     360
AGTCTCTCTCGGATGGTTTTACTTGGAGAAGAGTAAGCACSTATGACGATGGAGGAGTCC
S L S D G F T W R R V S T Y D D G G V L

     370     380     390     400     410     420
TCACAGTTACCCAAGACACTAGTCTGAAGGGAGATTGCATTATTTGCAACATTAAAGTCC
T V T Q D T S L K G D C I I C N I K V H

     430     440     450     460     470     480
ATGGCACTAACTTCCCCGAAAATGGTCCGGTGATGCAAAACAAGACCGATGGATGGGAGC
G T N F P E N G P V M Q N K T D G W E P

     490     500     510     520     530     540
CATCCAGCACTGAAACGGTTATTCCACAAGATGGAGGAATTGTTGCTGCGCGATCACCCG
S S T E T V I P Q D G G I V A A R S P A

     550     560     570     580     590     600
CACTAAGGCTGCGTGATAAAGGTCATCTTATCTGCCACATGGAACAACATTACAAGCCAA
L R L R D K G H L I C H M E T T Y K P N

     610     620     630     640     650     660
ACAAAGAGGTGAAGCTGCCAGAACTCCACTTTCATCATTGCGAATGGAAAAGCTGAGTG
K E V K L P E L H F H H L R M E K L S V

     670     680     690     700     710     720
TTAGTGACGATGGGAAGACCATTAAGCAGCACGAGTATGTGGTGGCTAGCTACTCCAAAG
S D D G K T I K Q H E Y V V A S Y S K V

     730     740     750     760     770     780
TGCCCTTCGAAGATAGGACGTCAATGATCATTTCCCTTATTAAATATCAATGATGTGGCTT
P S K I G R Q *

     790     800     810     820     830     840
TCAATTTTCCAAAATTTTGTTAAGACATAGGTCTTTTGGATTTTGGTAACCCCAACCTT
      850     860     870     880     890
AATTCCTCAATAATTTTGTGGAAAGTCAAATAAAACCAGCCTTCCCTGGGCCTTTAA 3'
(SEQ ID NOS: 19 & 20)
```

FIGURE 18

Green fluorescent protein from *Agaricia fragilis* afraGFP (AY037765)

```

      10      20      30      40      50      60
5'CAAGGAAGCCAAATCTTTTACCAGAGATCTCGCGTGAAGCAACCTATGAGTGATGGCGA
                                     M A I

      70      80      90      100     110     120
TTTCTACTCTAAAGACGTCAATCATCGTTATTATATACTCCTGCAGCACTTGTGCTG
S T L K N V I I I V I I Y S C S T C A V

     130     140     150     160     170     180
TTTGGTCGAATTCAAACCTCTGAATCCTCTTTCACTAATGGGATTGCAGAGGAAATGAAGA
W S N S N S E S S F T N G I A E E M K T

     190     200     210     220     230     240
CTAGGGTACATTTGGAGGGTACTGTTAACGGGCACTCCTTTACAATTAAAGGCGAAGGAA
R V H L E G T V N G H S F T I K G E G R

     250     260     270     280     290     300
GAGGCTACCCCTTACAAAGGAGAACAGTTTATGAGCCTTGAGGTCGTCATGGTGCTCCTC
G Y P Y K G E Q F M S L E V V N G A P L

     310     320     330     340     350     360
TGCCGTTCTCTTTTGATATCTTGACACCAGCATTTATGTATGGCAACAGAGTGTTACCA
P F S F D I L T P A F M Y G N R V F T K

     370     380     390     400     410     420
AGTACCCACCAACATACCAGACTATTCAAGCAGACGTTTCCTGAAGGGTATCACTGGG
Y P P N I P D Y F K Q T F P E G Y H W E

     430     440     450     460     470     480
AAAGAAACATTCCCTTTGAAGATCAGGCCGCGTGCACGGTAACCAGCCACATAAGATTGG
R N I P F E D Q A A C T V T S H I R L E

     490     500     510     520     530     540
AAGAGGAAGAGAGGCGTTTTTGTAATAACGTCAGATTTCACGTGTGTAACCTTCCCCCTA
E E E R R F V N N V R F H C V N F P P N

     550     560     570     580     590     600
ATGGTCCAGTCATGCAGAGGAGGATACTGAAATGGGAGCCATCCACTGAGAACATTTATC
G P V M Q R R I L K W E P S T E N I Y P

     610     620     630     640     650     660
CGCGTGATGGGTTTCTGGAGGGCCATGTTGATATGACTCTTCGGGTTGAAGGAGGTGGCT
R D G F L E G H V D M T L R V E G G G Y

     670     680     690     700     710     720
ATTACCGAGCTGAGTTCAAAAGTACTTACAAAGGGAAGACCCAGTCCGCGACATGCCAG
Y R A E F K S T Y K G K T P V R D M P D

     730     740     750     760     770     780
ACTTTCACCTTCATAGACCACCGCATTGAGATTACGGAGCATGACGAAGACTACACCAATG
F H F I D H R I E I T E H D E D Y T N V

     790     800     810     820     830     840
TTGAGCTGCATGACGTATCCTGGGCTCGTTACTCTATGCTGCCGACTATGTAAGCGGAAA
E L H D V S W A R Y S M L P T M

     850     860     870     880     890     900
AGGCAAGGCAACAAGACGCAAAACCGCCCTGTTTGTCTCTTTTCATAAGAGATTTGACAA
910     920     930     940     950     960
CCGTGGTTCTTTGCCATTTAATTTGAATTAGTTTAAATTAATCTTTGGGATTGATGTAG
970     980     990    1000    1010    1020
ACGCTTTGGTTGCTAAGTAAGAAAACATTTGTGATTATTAAATTTGTTGCCTGAAGCAAA
1030
AAAAAAAAA 3'
```

(SEQ ID NOS:21 & 22)

FIGURE 19

Green fluorescent protein from *Ricordea florida* rfloGFP2 (AY037774)

```

      10      20      30      40      50      60
5'AGCCACTTCGGTGTCTTGTGCGAGAGGAAGGATCACGAACAAGAGAAGAGCTGTAAAAGTT
      70      80      90     100     110     120
   AAAATTTTACTTTACTTCTTCCAGCATGAATGCACTTCAAGAGGAAATGAAAATCAAGCT
               M N A L Q E E M K I K L

      130     140     150     160     170     180
TACAATGGTGGGCGTTGTTAACGGGCAGTCATTTAAGATCGATGGGAAAGGAAAAGGGAA
   T M V G V V N G Q S F K I D G K G K G K

      190     200     210     220     230     240
ACCTTACGAGGGATCACAGGAATTGACCCTTAAAGTGGTGGAAGGCGGCCTCTGCTCTT
   P Y E G S Q E L T L K V V E G G P L L F

      250     260     270     280     290     300
CTCTTATGATATCCTGACAACGATATTTCAGTATGGCAACAGGGCATTCGTGAACTACCC
   S Y D I L T T I F Q Y G N R A F V N Y P

      310     320     330     340     350     360
AAAGGACATACCAGATATTTTCAAGCAAACGTGTTCTGGTCTTGATGGCGGATATTCGTG
   K D I P D I F K Q T C S G L D G G Y S W

      370     380     390     400     410     420
GCAAAGGACCATGACTTATGAGGACGGAGGGGTTTGTACTGCTACAAGCAACGTCAGCGT
   Q R T M T Y E D G G V C T A T S N V S V

      430     440     450     460     470     480
GGTCGGCGACACTTTCAATTATGAAATTCACCTTTATGGGGCGCAATTTCTCTCCAAATGG
   V G D T F N Y E I H F M G A N F P P N G

      490     500     510     520     530     540
TCCRGATGATGCAGAAAAGAACAGTGAAGTGGGAGCCCTCCACTGAGATAATGTTTGAACG
   P V M Q K R T V K W E P S T E I M F E R

      550     560     570     580     590     600
TGATGGATTGCTGAGGGGTGATGTTCCCATGTCTCTGTTGCTGAAAGGAGGCGACCATTA
   D G L L R G D V P M S L L L K G G D H Y

      610     620     630     640     650     660
CCGATGTGACTTTAAACTATTTATAAACCCAACAAGAAGGTCAAGCTGCCAGGTTACCA
   R C D F K T I Y K P N K K V K L P G Y H

      670     680     690     700     710     720
TTTTGTGGACCACTGCATTGAGATAAAGAGTCAAGAGAATGATTACAACATGGTTGCGCT
   F V D H C I E I K S Q E N D Y N M V A L

      730     740     750     760     770     780
CTTTGAGGATGCTGTAGCACACTACTCTCCTCTGGAGAAAAGAGCCAGGCAAAGGCGTA
   F E D A V A H Y S P L E K K S Q A K A *

      790     800     810     820     830     840
AATCCAAACAACCTAAGAAGACGACAAGGCATTCAATCTAATCGCATGTTTGAATTTTGT
   850     860     870     880     890     900
GTTAGGAATGTGTTGGGTCAGACTAGGTCTAGAACGTTTCATTTTGGCTGGATTGTTTT
   910     920     930     940     950     960
ACTCAGTTATAGACAAGAAAAAATCTTAAATGACTTGGGTTGGATTAGCTTTCGGGCAC
   970     980     990    1000    1010    1020
TGTCAAATCCGGATTCCCTTAGAAATATTTGAGACCAAGCCTTTTTTTGAGCTGAGAACGT

AATC 3'
```

(SEQ ID NOS: 23 & 24)

FIGURE 20

Green fluorescent protein from *Montastraea cavernosa* mcavGFP2 (AY037768)

```

      10      20      30      40      50      60
5'AGAGCTGTAGGGTGATATCTTACTTACGTCTACCATCATGACCAGTGTTCACAGGAAAA
      M T S V A Q E K

      70      80      90     100     110     120
GGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCA
      G V I K P D M K M K L R M E G A V N G H

      130     140     150     160     170     180
CAAGTTCGTGATTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGA
      K F V I E G D G K G K P F D G T Q T M D

      190     200     210     220     230     240
CCTTACAGTCATAGAAGGCGCACCATTTGCCTTTCGCTTACGCTATCTTGACAACAGTATT
      L T V I E G A P L P F A Y A I L T T V F

      250     260     270     280     290     300
CGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCA
      D Y G N R V F A K Y P E D I A D Y F K Q

      310     320     330     340     350     360
GACATTTCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTG
      T F P E G Y F W E R S M T Y E D Q G I C

      370     380     390     400     410     420
CATCGCCACAAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTTGTCTATAAAAT
      I A T N D I T M M K G V D D C F V Y K I

      430     440     450     460     470     480
TCGATTTGATGGTGTGAACCTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAA
      R F D G V N F P A N G P V M Q R K T L K

      490     500     510     520     530     540
ATGGGAGCCATCCACTGAGAAAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAA
      W E P S T E K M Y A R D G V L K G D V N

      550     560     570     580     590     600
CATGGCTCTGTGCTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAG
      M A L L L E G G G H Y R C D F K T T Y R

      610     620     630     640     650     660
AGCTAAGAAGGTTGTCCAGTTGCCAGACTATCATTGTGGACCATCGCATTGAGATTGT
      A K K V V Q L P D Y H F V D H R I E I V

      670     680     690     700     710     720
GAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCTGG
      S H D K D Y N K V K L Y E H A E A H S G

      730     740     750     760     770     780
GCTGCCGAGGCAGGCCAAGTAAAGGCTTAATGAAAAGCCAAGACGACAACAAGGAGAAAC
      L P R Q A K *

      790     800     810     820     830     840
AAAGTATTTTTTTGTTAAATTTCAAGGCATTTACTCGGAATTAGTATTTGATACTTTCG
      850     860     870     880     890     900
ATTCAAGGATTGTTTCGGGACTTGTTAGAGACGAGCTCTAGAGTTGATTTTGTGAAAA
      910
AAAGATAGTTTCC 3'

```

(SEQ ID NOS: 25 & 26)

FIGURE 21

Green fluorescent protein homolog from *Montastraea annularis* mannFP (AY037766)

```

      10      20      30      40      50      60
5'TGGTTAACGCAGAGTCGCGGGGGTTCCTGGCTAATAATTGATTCTATTTTGGGTGTGAC
      70      80      90     100     110     120
  ATTCAAGGTTTAAAGCAGCATCCTCAGTGGCTGAGGTCTCATTCACCCCTGGTGATTGGAAG
     130     140     150     160     170     180
  AGAGCAGATCGAGAACACCAAGAGCTGTATTACGCTAAATCTTACTTGCCTCTACCACC
     190     200     210     220     230     240
  ATGAGTATGATTAAACCAGAAATGAAGATCAAGATGCGTATGGACGGTGTCTGTAACGGG
  M S M I K P E M K I K M R M D G A V N G

      250     260     270     280     290     300
  CACAAGTTCGTGATTACAGGGGAAGGAAGCGGCGAGCCTTTCGAGGGAAAACAGACTATG
  H K F V I T G E G S G E P F E G K Q T M

      310     320     330     340     350     360
  AACCTGACAGTCATAGACGGCGGACCTCTGCCTTTCGCTTTCGACATCTTGACAACAGCA
  N L T V I D G G P L P F A F D I L T T A

      370     380     390     400     410     420
  TTCGATTACGGCAGGGTATTCGCCAAATACCCAGAAGACATCCAGACTATTTCAG
  F D Y G X R V F A K Y P E D I P D Y F K

      430     440     450     460     470     480
  CAGTCGTTTCTGAGGGGTTTCTTGGGAACGAAGCATGACTTACGAAGACGGGGGCATT
  Q S F P E G F S W E R S M T Y E D G G I

      490     500     510     520     530     540
  TGCATCGCCACAAATGACATAAAATGGAAGGCGACTGCTTTTCCTATGAAATTCGATT
  C I A T N D I K M E G D C F S Y E I R F

      550     560     570     580     590     600
  GATGGGGTGAACCTTTCCTGCCAATAGTCCAGTTATGCAGAAGAAGACCGTGAAATGGGAG
  D G V N F P A N S P V M Q K K T V K W E

      610     620     630     640     650     660
  CCATGCACTGRGGAATGTATGTGCGTGATGGAGTGCTTAAAGGTGGTCTTAAATGGCT
  P C T X E M Y V R D G V L K G G L N M A

      670     680     690     700     710     720
  CTGTTGCTTGAAGGAGGTGGCCATTTCGATGTGACTTGAAAACACTTACAAAGCTAAG
  L L L E G G G H F R C D L K T T Y K A K

      730     740     750     760     770     780
  AAGGTTGTCCAGATGCCAGACTATCACTTTGTGAATCACCGACTTGAGATAACATGGCAT
  K V V Q M P D Y H F V N H R L E I T W H

      790     800     810     820     830     840
  GACGAGGATTACAACATGTTAAGCTGTCTGAGCATGCAGAAGCTCATTCTGGACTGCCA
  D E D Y N N V K L S E H A E A H S G L P

      850     860     870     880     890     900
  AGGCAGGCCAAATAAGGCTTGACGAAAAGCCAAAACGGCAAAGAGTACAAGAAAGTATA
  R Q A K *

      910     920     930     940     950     960
  TATAAATGTATATTTTCAACTGAAAGGCATTCCACTCGGAATTAGTATTTGATACTTTC
     970     980     990    1000    1010    1020
  AATTCAAGGATTTATTTTGGGATTTGCTAGCCACTAGCTTTATTGTAAATTAAGTTAAA
    1030    1040    1050    1060    1070    1080
  GACGGTTTAGCATTTTTCGGTATTACAACATAGGCACAGACGTCTTAACCCAGTAGTG
    1090    1100    1110    1120    1130
  GTCAGGTACAAGTAAGAAACTTTGGTGAGAATAGACTTGTAGTCGAAAAAAA 3'

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(SEQ ID NOS:27 & 28)

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METHODS FOR USING THE SAME

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g a t a g t g t t a   g t g a c g a t g a   g a a g a c c a t t   g a g c a g c a c g   a g a a t g t g a g   g g c a a g c t a c   720
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c c a a a t t t t c   t t a g a c a c a g   t c t t t t c c t t   t a g c t t c g t a   g c c t a c t t a c   c c a t g t t t t g   840
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<213> Heteractis crispa

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      35             40             45
Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser His Ala Phe Arg Tyr
      50             55             60
Gly Asn Lys Val Phe Ala Lys Tyr Pro Lys Asp His Pro Asp Phe Phe
      65             70             75             80
Lys Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Val Ser Asn Tyr
      85             90             95
Glu Asp Gly Gly Val Leu Thr Val Lys Gln Glu Thr Ser Leu Glu Gly
      100            105            110

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Glu Thr Val Ile Pro Arg Gly Gly Gly Ile Leu Met Arg Asp Val Pro
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Ala Leu Lys Leu Leu Gly Asn Lys Gly His Leu Leu Cys Val Met Glu
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Thr Thr Tyr Lys Ser Lys Lys Lys Gly Glu Pro Ala Lys Pro His Phe
      180                      185                      190
His His Leu Arg Met Glu Lys Asp Ser Val Ser Asp Asp Glu Lys Thr
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      35                      40                      45
Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Ala Leu His Tyr Gly
      50                      55                      60
Asn Arg Val Phe Thr Glu Tyr Pro Ala Asp Ile Thr Asp Tyr Phe Lys
65                      70                      75                      80
Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Thr Tyr Glu
      85                      90                      95
Asp Lys Gly Ile Cys Thr Ile Arg Ser Asp Ile Ser Leu Glu Gly Asp
      100                      105                      110
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Tyr	Lys	Ala	Lys	Lys	Val	Val	Gln	Leu	Pro	Asp	Tyr	His	Phe	Val	Asp				
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Leu	Tyr	Glu	His	Gly	Val	Ala	Arg	Tyr	Ser	Pro	Leu	Pro	Lys	Ser	Gly				
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 35 40 45
 Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Ala
 50 55 60
 Phe Asp Tyr Gly Asn Arg Leu Phe Thr Glu Tyr Pro Glu Gly Ile Val
 65 70 75 80
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp His Arg Ser
 85 90 95
 Phe Arg Phe Glu Asp Gly Ala Val Cys Ile Cys Ser Ala Asp Ile Thr
 100 105 110
 Val Asn Val Arg Glu Asn Cys Ile Tyr His Glu Ser Thr Phe Tyr Gly
 115 120 125

Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Thr	Asn
130						135					140				
Trp	Glu	Pro	Ser	Cys	Glu	Lys	Ile	Ile	Pro	Ile	Asn	Ser	Gln	Lys	Ile
145					150					155					160
Leu	Lys	Gly	Asp	Val	Ser	Met	Tyr	Leu	Leu	Lys	Asp	Gly	Gly	Arg	
				165				170					175		
Tyr	Arg	Cys	Gln	Phe	Asp	Thr	Ile	Tyr	Lys	Ala	Lys	Thr	Glu	Pro	Lys
			180					185					190		
Glu	Met	Pro	Asp	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Asn	Arg	Glu	Asp
	195						200					205			
Arg	Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	Gln	Leu	Ile	Glu	His	Ala	Ile
	210					215					220				
Ala	Ser	Arg	Ser	Ala	Leu	Pro									
225					230										

<210> 7

<211> 1178

<212> DNA

<213> Scolymia cubensis

<400> 7

tgtgacattc	agtcatatag	gagcctctat	cggagctgag	gtccattca	ccgttgtgat	60
ttggacggga	gcagatcgag	aacaacmagg	gctgtacgag	tctgataatt	tactttacat	120
ctaccaacat	gcagcgtgct	gggatgaagg	ttaaggaaca	tatgaagatc	aaactgacga	180
tgggagggtac	tgtaaaccgga	aagcatttctg	cgggttaatgg	gacaggagac	ggctaccctt	240
atcaggggaaa	acagatttttg	aaacttatcg	tcgaaggcag	cgaacctctg	cctttcgctt	300
ttgatatcctt	gtcagcagca	ttccagtatg	gcaacagggc	attcaccgaa	taccaaacag	360
agatagcaga	ctatttcaag	cagtcgtttg	agtttggcga	ggggttctcc	tgggaacgaa	420
gtttcactttt	cgaagatggg	gccatttgcg	tcgccaccaa	cgatataacg	atggttgggtg	480
gtgagtttca	gtatgatatt	cgatttgatg	gtctgaactt	ccctgaagat	gggccagtga	540
tgcaaaagaa	aaccgtaaaa	tgggagccat	ccactgagat	aatgtatatg	caaaatggag	600
tgctgaaggg	tgagggttaac	atggctctgt	tgcttcaaga	caaaagccat	taccgttgcg	660
acctcaaaac	tacttacaaa	gctaagaata	atgtgccgca	tcctccaggc	taccactatg	720
tggatcactg	cattgaaata	ctcgaagaac	gtaaggatca	cgtaagctg	cgggagcatg	780
ctaaagctcg	ttctagcctg	tcacctacca	gtgcaaaaga	acgaaaggct	taggtgatag	840
tcaaaaagac	aacaagacga	aaatgaaagg	tgttcattgt	tagaatttga	tattttcgat	900
tcaatgatc	gttaagggat	ttgctagagg	ctagctaaca	ggtaacatc	ataaggatag	960
agattycgtt	gcggagttag	aaccttwata	ttttccgaat	tccamctaga	gtcgttgaga	1020
aattttattag	agactagctt	tagagttact	tttgtggaaa	aaaaggtttc	cattttttgc	1080
gttattacag	cattttaaagc	ataggaatag	agattcgggtt	atggaaaata	acagtaggaa	1140
aatacgttgt	gaaaataaac	ttgtttgtcga	aaaaaaaa			1178

<210> 8

<211> 234

<212> PRT

<213> Scolymia cubensis

<400> 8

Met	Gln	Arg	Ala	Gly	Met	Lys	Val	Lys	Glu	His	Met	Lys	Ile	Lys	Leu
1				5				10					15		
Arg	Met	Gly	Gly	Thr	Val	Asn	Gly	Lys	His	Phe	Ala	Val	Asn	Gly	Thr
		20					25					30			
Gly	Asp	Gly	Tyr	Pro	Tyr	Gln	Gly	Lys	Gln	Ile	Leu	Lys	Leu	Ile	Val
		35				40					45				
Glu	Gly	Ser	Glu	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ser	Ala	Ala
	50					55				60					
Phe	Gln	Tyr	Gly	Asn	Arg	Ala	Phe	Thr	Glu	Tyr	Pro	Thr	Glu	Ile	Ala
	65			70				75						80	
Asp	Tyr	Phe	Lys	Gln	Ser	Phe	Glu	Phe	Gly	Glu	Gly	Phe	Ser	Trp	Glu
			85					90						95	

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Arg Ser Phe Thr Phe Glu Asp Gly Ala Ile Cys Val Ala Thr Asn Asp
      100                      105                      110
Ile Thr Met Val Gly Gly Glu Phe Gln Tyr Asp Ile Arg Phe Asp Gly
      115                      120                      125
Leu Asn Phe Pro Glu Asp Gly Pro Val Met Gln Lys Lys Thr Val Lys
      130                      135                      140
Trp Glu Pro Ser Thr Glu Ile Met Tyr Met Gln Asn Gly Val Leu Lys
      145                      150                      155                      160
Gly Glu Val Asn Met Ala Leu Leu Leu Gln Asp Lys Ser His Tyr Arg
      165                      170                      175
Cys Asp Leu Lys Thr Thr Tyr Lys Ala Lys Asn Asn Val Pro His Pro
      180                      185                      190
Pro Gly Tyr His Tyr Val Asp His Cys Ile Glu Ile Leu Glu Glu Arg
      195                      200                      205
Lys Asp His Val Lys Leu Arg Glu His Ala Lys Ala Arg Ser Ser Leu
      210                      215                      220
Ser Pro Thr Ser Ala Lys Glu Arg Lys Ala
      225                      230

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<210> 9
 <211> 819
 <212> DNA
 <213> Scolymia cubensis

```

<400> 9
cctggtgatt tggacgagag cagatcgaga atagcaaggt tttaccagcg tgataattta 60
ctttacatct aacaacatgc aatctgctgg gaagaagaat gtcgttaagg acttcatgaa 120
gatcacactg cgtatggacg gtgctgtaaa cggaagccc ttgcggtta atggaacagg 180
agatggcaac ccttatggtg gaatacacagag tttgaagctt accgtcgatg gcaacaaacc 240
tctgcctttt gcttttgata tcttgtcagc agcattccag tatggcaaca gggcattcac 300
cgaataccca aaagagatat cagactatct caagcagtcg tttgagtttg gcgaggggtt 360
tacctgggaa cgaagtttca ctttcgaaga cggggccatt tgcgtcgcca cgaacgatat 420
aaagatgggt ggcatgagt ttcaatataa cattcgattt gatggtgtga atttccctga 480
agatggtccw gtyatgcaga agaaaacggg gaagtgggag ccacccacag agataatgcg 540
tgtgcaaggt ggagtgctaa agggtgaggt taacatggct ctgttgctta aagacaaaag 600
ccattaccga tgtgacttca aaactactta caaagctaag aatcctgtcc cgccgacggc 660
gcttccagac taccactatg tggatcactg tattgaaatc accgaggaaa atagggatta 720
cgtaagctg caggagtatg ctaaaagctc ttctggcctg cacctgcccg aactgcaaaa 780
gtaaaggctt aggcgatagt caagacgaca acgagaaga 819

```

<210> 10
 <211> 235
 <212> PRT
 <213> Scolymia cubensis

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<400> 10
Met Gln Ser Ala Gly Lys Lys Asn Val Val Lys Asp Phe Met Lys Ile
  1      5      10      15
Thr Leu Arg Met Asp Gly Ala Val Asn Gly Lys Pro Phe Ala Val Asn
  20      25      30
Gly Thr Gly Asp Gly Asn Pro Tyr Gly Gly Ile Gln Ser Leu Lys Leu
  35      40      45
Thr Val Asp Gly Asn Lys Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser
  50      55      60
Ala Ala Phe Gln Tyr Gly Asn Arg Ala Phe Thr Glu Tyr Pro Lys Glu
  65      70      75      80
Ile Ser Asp Tyr Phe Lys Gln Ser Phe Glu Phe Gly Glu Gly Phe Thr
  85      90      95
Trp Glu Arg Ser Phe Thr Phe Glu Asp Gly Ala Ile Cys Val Ala Thr
  100     105     110

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Asn Asp Ile Lys Met Val Gly Asp Glu Phe Gln Tyr Asn Ile Arg Phe
    115                      120                      125
Asp Gly Val Asn Phe Pro Glu Asp Gly Pro Val Met Gln Lys Lys Thr
    130                      135                      140
Val Lys Trp Glu Pro Ser Thr Glu Ile Met Arg Val Gln Gly Gly Val
    145                      150                      155                      160
Leu Lys Gly Glu Val Asn Met Ala Leu Leu Leu Lys Asp Lys Ser His
    165                      170                      175
Tyr Arg Cys Asp Phe Lys Thr Thr Tyr Lys Ala Lys Asn Pro Val Pro
    180                      185                      190
Pro Thr Ala Leu Pro Asp Tyr His Tyr Val Asp His Cys Ile Glu Ile
    195                      200                      205
Thr Glu Glu Asn Arg Asp Tyr Val Lys Leu Gln Glu Tyr Ala Lys Ala
    210                      215                      220
Arg Ser Gly Leu His Leu Pro Glu Leu Gln Lys
    225                      230                      235

```

<210> 11
 <211> 807
 <212> DNA
 <213> Ricordea florida

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<400> 11
tgtgaaagtt aacattttac tttacttcta ccagcatgag tgcactcaaa gaggaaatga 60
aaatcaagct tacattgggtg ggcgttggtta acgggcaccc attcaagatc attggggacg 120
gaaaaggcaa accctatgag ggatcgcagg aattaaccct tgccgtgggtg gaaggagggc 180
ctctgccttt ctcttatgat atcctgacaa cgatagttca ctatggcaac agggcatttg 240
tgaactaccc aaaggacata ccagatatatt tcaagcagac ctgctctggt cctgggtgctg 300
gatattcctg gcaaaaggacc atgagttttg aagacggagg cgtttgcaact gctacgagcc 360
atatcagggt ggatggcgac actiltcaatt atgacattca cttcatggga gcggatttcc 420
ctcttaaatg tccagtgatg cagaaaagaa cagtgaatg ggagccatcc actgagataa 480
tgtttcaatg tgaatggaltg ctgaggggtg atgttgccat gtctctgttg ctgaaaggag 540
gcggccatta ccgatgtgac tttaaaacta tttataaacc caagaagaat gtcaagatgc 600
caggttacca ttttgtggac cactgcattg agataacgag tcaacaggac gattacaacg 660
tggttgagct gtacgagggt gctgtagccc actactctcc tctgcagaaa ccatgccaaag 720
caaaggcata aagccaaaca acccaagagg acaacaagac atttaatcaa atcacatctt 780
tgtatttttg gttagagttg aaaaaaaa

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<210> 12
 <211> 231
 <212> PRT
 <213> Ricordea florida

```

<400> 12
Met Ser Ala Leu Lys Glu Glu Met Lys Ile Lys Leu Thr Leu Val Gly
    1           5           10           15
Val Val Asn Gly His Pro Phe Lys Ile Ile Gly Asp Gly Lys Gly Lys
    20           25           30
Pro Tyr Glu Gly Ser Gln Glu Leu Thr Leu Ala Val Val Glu Gly Gly
    35           40           45
Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Ile Val His Tyr Gly
    50           55           60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
    65           70           75           80
Gln Thr Cys Ser Gly Pro Gly Ala Gly Tyr Ser Trp Gln Arg Thr Met
    85           90           95
Ser Phe Glu Asp Gly Gly Val Cys Thr Ala Thr Ser His Ile Arg Val
    100          105          110
Asp Gly Asp Thr Phe Asn Tyr Asp Ile His Phe Met Gly Ala Asp Phe
    115          120          125

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Pro Leu Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
 130                      135                      140
Ser Thr Glu Ile Met Phe Gln Cys Asp Gly Leu Leu Arg Gly Asp Val
 145                      150                      155                      160
Ala Met Ser Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe
                      165                      170                      175
Lys Thr Ile Tyr Lys Pro Lys Lys Asn Val Lys Met Pro Gly Tyr His
                      180                      185                      190
Phe Val Asp His Cys Ile Glu Ile Thr Ser Gln Gln Asp Asp Tyr Asn
                      195                      200                      205
Val Val Glu Leu Tyr Glu Gly Ala Val Ala His Tyr Ser Pro Leu Gln
                      210                      215                      220
Lys Pro Cys Gln Ala Lys Ala
 225                      230

```

<210> 13
 <211> 796
 <212> DNA
 <213> Ricordea florida

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<400> 13
agtcacctcg gtgttttttag gacaggaagg atcacgagca agagaagaac tgtgaaagtt 60
aacactttac tctacttcta ccagcatgag tgcactcaaa gaggaatga aaatcaagct 120
taaaatggtg ggcgttgta acgggcagtc atttcagatc gatggggaag gaaaaggcaa 180
accttacgag ggatcacaga aattaaccct tgaagtgggt gaaggagggc ctctgctctt 240
ctcttatgat atcctgacaa cgataatttca gtatggcaac agggcattcg tgaactaccc 300
aaaggacata ccagatatatt tcaagcagac ctgctctggt cctgatgggt gattttcctg 360
gcaaaggacc atgacttatg aagacggagg ggtttgact gcttcaaacc acatcagcgt 420
ggacggcgac actttttatt atgtgataag atttaattga gagaattttc ctccaaatgg 480
tccagtaatg cagaaaagaa cagtgaatg ggagccatcc actgagataa tgtttgaacg 540
tgatggattg ctgaggggtg acattgccat gtctctgttg ctgaaaggag gcggccatta 600
ccgatgtgac tttaaaacta tttatacacc caagaggaag gtcaacatgc caggttacca 660
ttttgtggac cactgcattg agatacagaa gcacgacaag gattacaaca tggctgtgct 720
ctctgaggat gctgtagccc acaactctcc tctggagaaa aaaagccaag caaaggcgta 780
aagccaaaca acctaa 796

```

<210> 14
 <211> 231
 <212> PRT
 <213> Ricordea florida

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<400> 14
Met Ser Ala Leu Lys Glu Glu Met Lys Ile Lys Leu Lys Met Val Gly
 1                      5                      10                      15
Val Val Asn Gly Gln Ser Phe Gln Ile Asp Gly Glu Gly Lys Gly Lys
                      20                      25                      30
Pro Tyr Glu Gly Ser Gln Lys Leu Thr Leu Glu Val Val Glu Gly Gly
                      35                      40                      45
Pro Leu Leu Phe Ser Tyr Asp Ile Leu Thr Thr Ile Phe Gln Tyr Gly
                      50                      55                      60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
 65                      70                      75                      80
Gln Thr Cys Ser Gly Pro Asp Gly Gly Phe Ser Trp Gln Arg Thr Met
                      85                      90                      95
Thr Tyr Glu Asp Gly Gly Val Cys Thr Ala Ser Asn His Ile Ser Val
                      100                     105                     110
Asp Gly Asp Thr Phe Tyr Tyr Val Ile Arg Phe Asn Gly Glu Asn Phe
                      115                     120                     125
Pro Pro Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
                      130                     135                     140

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Ser Thr Glu Ile Met Phe Glu Arg Asp Gly Leu Leu Arg Gly Asp Ile
 145 150 155 160
 Ala Met Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe
 165 170 175
 Lys Thr Ile Tyr Thr Pro Lys Arg Lys Val Asn Met Pro Gly Tyr His
 180 185 190
 Phe Val Asp His Cys Ile Glu Ile Gln Lys His Asp Lys Asp Tyr Asn
 195 200 205
 Met Ala Val Leu Ser Glu Asp Ala Val Ala His Asn Ser Pro Leu Glu
 210 215 220
 Lys Lys Ser Gln Ala Lys Ala
 225 230

<210> 15

<211> 795

<212> DNA

<213> Montastraea cavernosa

<400> 15

acgcagggat tcaccctggt gattttggaag agagcagacc gagaacaaca agagctgtat 60
 aaggctgata tcttacttta cgtctaccat catgagtgtg attaaatcag tcatgaagat 120
 caagctgcgt atggaaggca gtgtaaacgg gcacaacttc gtaattgttg gagaaggaga 180
 aggcaagcct tatgagggaa cacagagtat ggaccttaca gtcaaagaag gcgcacctct 240
 gcctttcgcc tacgatatca tgacaacagt attccattac ggcaataggg tattcgcaaa 300
 atacccaaaa catatcccag actattttcaa gcagatgttt cctgaggagt attcctggga 360
 acgaagcatg aatttcgaag gcgggggcat ttgcaccgcc aggaacgaga taacaatgga 420
 aggcgactgt tttttcaata aagttcgatt tgatggtgtg aacttcccc ccaatgggcc 480
 agtcatgcag aagaagacgc tgaaatggga gccatccact gaaaaaatgt atgtgcgtga 540
 tggagtgtctg acgggtgata tcaacatggc tttgttgctt gaaggagggt gccattaccg 600
 atgtgacttc agaactactt acagagctaa gaagaagggt gtcaagttac cagattatca 660
 ctttgaggat cactccattg agattttgcg ccatgacaaa gaatacactg aggttaagct 720
 gtatgagcat gccgaagctc attctgggct gccgagggtg gcaaagtaaa ggcttaacga 780
 aaagccaaga ccaca 795

<210> 16

<211> 235

<212> PRT

<213> Montastraea cavernosa

<400> 16

Arg Leu Ile Ser Tyr Phe Thr Ser Thr Ile Met Ser Val Ile Lys Ser
 1 5 10 15
 Val Met Lys Ile Lys Leu Arg Met Glu Gly Ser Val Asn Gly His Asn
 20 25 30
 Phe Val Ile Val Gly Glu Gly Glu Gly Lys Pro Tyr Glu Gly Thr Gln
 35 40 45
 Ser Met Asp Leu Thr Val Lys Glu Gly Ala Pro Leu Pro Phe Ala Tyr
 50 55 60
 Asp Ile Met Thr Thr Val Phe His Tyr Gly Asn Arg Val Phe Ala Lys
 65 70 75 80
 Tyr Pro Lys His Ile Pro Asp Tyr Phe Lys Gln Met Phe Pro Glu Glu
 85 90 95
 Tyr Ser Trp Glu Arg Ser Met Asn Phe Glu Gly Gly Gly Ile Cys Thr
 100 105 110
 Ala Arg Asn Glu Ile Thr Met Glu Gly Asp Cys Phe Phe Asn Lys Val
 115 120 125
 Arg Phe Asp Gly Val Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys
 130 135 140
 Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Lys Met Tyr Val Arg Asp
 145 150 155 160

Gly	Val	Leu	Thr	Gly	Asp	Ile	Asn	Met	Ala	Leu	Leu	Leu	Glu	Gly	Gly
				165					170					175	
Gly	His	Tyr	Arg	Cys	Asp	Phe	Arg	Thr	Thr	Tyr	Arg	Ala	Lys	Lys	Lys
			180					185					190		
Gly	Val	Lys	Leu	Pro	Asp	Tyr	His	Phe	Glu	Asp	His	Ser	Ile	Glu	Ile
		195					200					205			
Leu	Arg	His	Asp	Lys	Glu	Tyr	Thr	Glu	Val	Lys	Leu	Tyr	Glu	His	Ala
	210					215					220				
Glu	Ala	His	Ser	Gly	Leu	Pro	Arg	Val	Ala	Lys					
225					230					235					

<210> 17
 <211> 1066
 <212> DNA
 <213> Montastraea cavernosa

<400> 17
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 tcttacttac gtctaccatc atgacaagtg ttgcacagga aaagggtgtg attaaaccag 120
 acatgaagat gaagctgcgt atggaagggtg ctgtaaacgg gcacaagttc gtggttgaag 180
 gagatggaaa aggggaagcct ttcgacggaa cacagactat ggaccttaca gtcatagaag 240
 gcgcaccatt gcccttcgct tacgatatct tgacaacagt attcgattac ggcaacaggg 300
 tattcgccaa ataccagaa gacatagcag attatttcaa gcagacgttt cctgaggggt 360
 acttctggga acgaagcatg acatacgaag accagggcat ttgcatcgcc acaaacgaca 420
 taacaatgat ggaaggcgtc gacgactgtt ttgcctataa aattcgattt gatggtgtga 480
 actttcctgc caatggtcca gttatgcaga ggaagacgct gaaatgggag ccatccactg 540
 agataatgta tgcgcgtgat ggagtgtga agggtgatgt taacatggct ctggtgcttg 600
 aaggaggtag ccattaccga tgtgacttca aaactactta caaagctaag aaggttgtcc 660
 gggtgccaga ctatcacttt gtggaccatc gcattgagat tgtgagccac gacaaagatt 720
 acaacaagggt taagctgcac gagcatgccg aagctcgtca tggactgtca aggaaggcca 780
 agtaaaggct taatgaaaag tcaagacgac aacgaggaga aacaaagtac ttttttgta 840
 aatttgaagg catctactcg gaattagat ttgatacttt cgattcaagg atttggtccg 900
 ggatttgta gagactagct ctagagttgt attttgtgaa aaaagatagt ttccagtttt 960
 tgcgggatta cagcatgggg atagactttt taaactcagt tgtggtcaaa tgcaagtaag 1020
 aaaactgtag tgagaataaa cttgttatcg aagccgaaaa aaaaaa 1066

<210> 18
 <211> 234
 <212> PRT
 <213> Montastraea cavernosa

<400> 18
 Met Thr Ser Val Ala Gln Glu Lys Gly Val Ile Lys Pro Asp Met Lys
 1 5 10 15
 Met Lys Leu Arg Met Glu Gly Ala Val Asn Gly His Lys Phe Val Val
 20 25 30
 Glu Gly Asp Gly Lys Gly Lys Pro Phe Asp Gly Thr Gln Thr Met Asp
 35 40 45
 Leu Thr Val Ile Glu Gly Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu
 50 55 60
 Thr Thr Val Phe Asp Tyr Gly Asn Arg Val Phe Ala Lys Tyr Pro Glu
 65 70 75 80
 Asp Ile Ala Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr Phe Trp
 85 90 95
 Glu Arg Ser Met Thr Tyr Glu Asp Gln Gly Ile Cys Ile Ala Thr Asn
 100 105 110
 Asp Ile Thr Met Met Glu Gly Val Asp Asp Cys Phe Ala Tyr Lys Ile
 115 120 125
 Arg Phe Asp Gly Val Asn Phe Pro Ala Asn Gly Pro Val Met Gln Arg
 130 135 140

Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Ile Met Tyr Ala Arg Asp
 145 150 155 160
 Gly Val Leu Lys Gly Asp Val Asn Met Ala Leu Leu Leu Glu Gly Gly
 165 170 175
 Gly His Tyr Arg Cys Asp Phe Lys Thr Tyr Lys Ala Lys Lys Val
 180 185 190
 Val Arg Leu Pro Asp Tyr His Phe Val Asp His Arg Ile Glu Ile Val
 195 200 205
 Ser His Asp Lys Asp Tyr Asn Lys Val Lys Leu His Glu His Ala Glu
 210 215 220
 Ala Arg His Gly Leu Ser Arg Lys Ala Lys
 225 230

<210> 19

<211> 898

<212> DNA

<213> *Condylactis gigantea*

<400> 19

acagctgttc atccacgctc attcaagacg ccgtcaactt tattccagtc aggaaaatgt 60
 atccttggat caaggaaaacc atgcgcagta aggtttacat ggaaggagat gttaacaacc 120
 acgccttcaa gtgcaactgca gtaggagaag gaaaaccata caaaggctca caagacctga 180
 cgattaccgt cactgaagga ggtcctctgc catttgcttt cgacattctt tcacacgcct 240
 ttccagtatgg caacaagggtg ttcaccgatt accccgacga tattcctgat ttctttaagc 300
 agtctctctc ggatgggtttt acttggagaa gagtaagcac statgacgat ggaggagtcc 360
 tcacagttac ccaagacact agtctgaagg gagattgcat tatttgcaac attaaagtcc 420
 atggcactaa cttccccgaa aatgggtccgg tgatgcaaaa caagaccgat ggatgggagc 480
 catccagcac tgaaacggtt attccacaag atggaggaat tgttgctgcg cgatcacccg 540
 cactaagggt gcggtgataaa ggtcatctta tctgccacat ggaaacaact tacaagccaa 600
 acaaagaggt gaagctgcc aactccact ttcattcatt gcgaatggaa aagctgagtg 660
 ttagtgacga tgggaagacc attaagcagc acgagtatgt ggtggctagc tactccaaag 720
 tgccttcgaa gataggacgt caatgatcat ttcccttatt aaatatcaat gatgtggctt 780
 tcaattttcc aaaattttgt taagacatag gtcttttggg tttttggtaa cccaacctt 840
 aattcccaat aatttttgtt ggaaagtcaa ataaaaccag ccttccttgg gcctttaa 898

<210> 20

<211> 229

<212> PRT

<213> *Condylactis gigantea*

<400> 20

Met Tyr Pro Trp Ile Lys Glu Thr Met Arg Ser Lys Val Tyr Met Glu
 1 5 10 15
 Gly Asp Val Asn Asn His Ala Phe Lys Cys Thr Ala Val Gly Glu Gly
 20 25 30
 Lys Pro Tyr Lys Gly Ser Gln Asp Leu Thr Ile Thr Val Thr Glu Gly
 35 40 45
 Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser His Ala Phe Gln Tyr
 50 55 60
 Gly Asn Lys Val Phe Thr Asp Tyr Pro Asp Asp Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Leu Ser Asp Gly Phe Thr Trp Arg Arg Val Ser Thr Tyr
 85 90 95
 Asp Asp Gly Gly Val Leu Thr Val Thr Gln Asp Thr Ser Leu Lys Gly
 100 105 110
 Asp Cys Ile Ile Cys Asn Ile Lys Val His Gly Thr Asn Phe Pro Glu
 115 120 125
 Asn Gly Pro Val Met Gln Asn Lys Thr Asp Gly Trp Glu Pro Ser Ser
 130 135 140
 Thr Glu Thr Val Ile Pro Gln Asp Gly Gly Ile Val Ala Ala Arg Ser

```

145          150          155          160
Pro Ala Leu Arg Leu Arg Asp Lys Gly His Leu Ile Cys His Met Glu
          165          170          175
Thr Thr Tyr Lys Pro Asn Lys Glu Val Lys Leu Pro Glu Leu His Phe
          180          185          190
His His Leu Arg Met Glu Lys Leu Ser Val Ser Asp Asp Gly Lys Thr
          195          200          205
Ile Lys Gln His Glu Tyr Val Val Ala Ser Tyr Ser Lys Val Pro Ser
          210          215          220
Lys Ile Gly Arg Gln
225

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<210> 21
<211> 1030
<212> DNA
<213> Agaricia fragilis

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<400> 21
caaggaagcc aaatctttta ccagagatct cgcgtgaaag caacctatga gtgatggcga 60
tttctactct aaagaacgtc atcatcatcg ttattatata ctctgcagc acttgtgctg 120
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ctagggtaca tttggagggt actgttaacg ggcactcctt tacaattaaa ggcaaggaa 240
gaggctaccc ttacaaagga gaacagttta tgagccttga ggtcgtcaat ggtgctcctc 300
tgccgttctc ttttgatatc ttgacaccag catttatgta tggcaacaga gtgttcacca 360
agtaccaccc aaacatacca gactatttca agcagacgtt tcctgaaggg tatcactggg 420
aaagaaacat tccctttgaa gatcaggccg cgtgcacggt aaccagccac ataagattgg 480
aagaggaaga gaggcgtttt gtaaataacg tcagatttca ctgtgtgaac tttcccccta 540
atggtccagt catgcagagg aggatactga aatgggagcc atccactgag aacatttatc 600
cgcgtgatgg gtttctggag ggccatgttg atatgactct tcgggttgaa ggagggtggc 660
attaccgagc tgagttcaaa agtacttaca aagggaagac cccagtcgcg gacatgccag 720
actttcactt catagaccac cgcattgaga ttacggagca tgacgaagac tacaccaatg 780
ttgagctgca tgacgtatcc tgggctcgtt actctatgct gccgactatg taagcggaaa 840
aggcaaggca acaagacgca aaaccgccct gtttgtctct tttcataaga gatttgacaa 900
ccgtggttct ttgccattta atttgaatta gtttaaatta aatctttggg attgatgtag 960
acgctttggt tgctaagtaa gaaaacattt gtgattatta aatttgttgc ctgaagcaaa 1020
aaaaaaaaaa 1030

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<210> 22
<211> 259
<212> PRT
<213> Agaricia fragilis

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<400> 22
Met Ala Ile Ser Thr Leu Lys Asn Val Ile Ile Ile Val Ile Ile Tyr
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Ser Cys Ser Thr Cys Ala Val Trp Ser Asn Ser Asn Ser Glu Ser Ser
          20          25          30
Phe Thr Asn Gly Ile Ala Glu Glu Met Lys Thr Arg Val His Leu Glu
          35          40          45
Gly Thr Val Asn Gly His Ser Phe Thr Ile Lys Gly Glu Gly Arg Gly
          50          55          60
Tyr Pro Tyr Lys Gly Glu Gln Phe Met Ser Leu Glu Val Val Asn Gly
          65          70          75          80
Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr
          85          90          95
Gly Asn Arg Val Phe Thr Lys Tyr Pro Pro Asn Ile Pro Asp Tyr Phe
          100          105          110
Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Asn Ile Pro Phe
          115          120          125
Glu Asp Gln Ala Ala Cys Thr Val Thr Ser His Ile Arg Leu Glu Glu

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130	135	140
Glu Glu Arg Arg Phe Val Asn Asn Val Arg Phe	His Cys Val Asn Phe	
145	150	155
Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile	Leu Lys Trp Glu Pro	160
	165	170
Ser Thr Glu Asn Ile Tyr Pro Arg Asp Gly Phe	Leu Glu Gly His Val	175
	180	185
Asp Met Thr Leu Arg Val Glu Gly Gly Gly Tyr	Tyr Arg Ala Glu Phe	190
	195	200
Lys Ser Thr Tyr Lys Gly Lys Thr Pro Val Arg	Asp Met Pro Asp Phe	205
	210	215
His Phe Ile Asp His Arg Ile Glu Ile Thr Glu	His Asp Glu Asp Tyr	220
225	230	235
Thr Asn Val Glu Leu His Asp Val Ser Trp	Ala Arg Tyr Ser Met Leu	240
	245	250
Pro Thr Met		255

<210> 23
 <211> 1024
 <212> DNA
 <213> Ricordea florida

<400> 23
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 aaaatttttac tttacttctt ccagcatgaa tgcacttcaa gaggaaatga aaatcaagct 120
 tacaatggtg ggcgttggtta acgggcagtc atttaagatc gatgggaaag gaaaaggga 180
 accttacgag ggatcacagg aattgacct taaagtgggt gaaggcgggc ctctgctctt 240
 ctcttatgat atcctgacaa cgatatctca gtatggcaac agggcattcg tgaactaccc 300
 aaaggacata ccagatatct tcaagcaaac gtgttcttgt cttgatggcg gatattcgtg 360
 gcaaaggacc atgacttatg aggacggagg ggtttgtact gctacaagca acgtcagcgt 420
 ggtcggcgac actttcaatt atgaaattca ctttatgggg gcgaattttc ctccaaatgg 480
 tccrgtgatg cagaaaagaa cagtgaagtg ggagccctcc actgagataa tgtttgaacg 540
 tgatggattg ctgaggggtg atgttcccat gtctctgttg ctgaaaggag gcgaccatta 600
 ccgatgtgac tttaaaacta tttataaacc caacaagaag gtcaagctgc caggttacca 660
 ttttgtggac cactgcattg agataaagag tcaagagaat gattacaaca tggttgcgct 720
 ctttgaggat gctgtagcac actactctcc tctggagaaa aagagccagg caaaggcgta 780
 aatccaaaca acctaagaag acgacaaggc attcaatcta atcgcatgtt tgaatttttg 840
 gttaggaatg tgttgggtca gactaggtct agaacgtttc attttggctg gatttgtttt 900
 actcagttat agacaagaaa aaaatcttaa atgacttggg ttggatttag ctttcggcac 960
 tgtcaattcc ggattcctta gaaatatitg agaccaagcc tttttttgag ctgagaacgt 1020
 aatc 1024

<210> 24
 <211> 231
 <212> PRT
 <213> Ricordea florida

<400> 24
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 Val Val Asn Gly Gln Ser Phe Lys Ile Asp Gly Lys Gly Lys Gly Lys
 20 25 30
 Pro Tyr Glu Gly Ser Gln Glu Leu Thr Leu Lys Val Val Glu Gly Gly
 35 40 45
 Pro Leu Leu Phe Ser Tyr Asp Ile Leu Thr Thr Ile Phe Gln Tyr Gly
 50 55 60
 Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
 65 70 75 80
 Gln Thr Cys Ser Gly Leu Asp Gly Gly Tyr Ser Trp Gln Arg Thr Met

				85					90					95					
Thr	Tyr	Glu	Asp	Gly	Gly	Val	Cys	Thr	Ala	Thr	Ser	Asn	Val	Ser	Val				
			100					105					110						
Val	Gly	Asp	Thr	Phe	Asn	Tyr	Glu	Ile	His	Phe	Met	Gly	Ala	Asn	Phe				
		115					120					125							
Pro	Pro	Asn	Gly	Pro	Val	Met	Gln	Lys	Arg	Thr	Val	Lys	Trp	Glu	Pro				
	130					135					140								
Ser	Thr	Glu	Ile	Met	Phe	Glu	Arg	Asp	Gly	Leu	Leu	Arg	Gly	Asp	Val				
145					150					155					160				
Pro	Met	Ser	Leu	Leu	Leu	Lys	Gly	Gly	Asp	His	Tyr	Arg	Cys	Asp	Phe				
			165					170						175					
Lys	Thr	Ile	Tyr	Lys	Pro	Asn	Lys	Lys	Val	Lys	Leu	Pro	Gly	Tyr	His				
		180						185					190						
Phe	Val	Asp	His	Cys	Ile	Glu	Ile	Lys	Ser	Gln	Glu	Asn	Asp	Tyr	Asn				
		195					200					205							
Met	Val	Ala	Leu	Phe	Glu	Asp	Ala	Val	Ala	His	Tyr	Ser	Pro	Leu	Glu				
	210					215					220								
Lys	Lys	Ser	Gln	Ala	Lys	Ala													
225					230														

<210> 25

<211> 913

<212> DNA

<213> Montastraea cavernosa

<400> 25

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caagttcgtg attgaaggag atggaaaagg gaagcctttc gacggaacac agactatgga 180
ccttacagtc atagaaggcg caccattgcc tttcgcttac gctatcttga caacagtatt 240
cgattacggc aacagggtat tcgcaaata ccagaagac atagcagatt atttcaagca 300
gacatttcct gaggggtact tctgggaacy aagcatgaca tacgaagacc agggcatttg 360
catcgccaca aacgacataa caatgatgaa aggcgtcgac gactgttttg tctataaaat 420
tcgatttgat ggtgtgaact ttcctgccaa tgggccagtt atgcagagga agacgctgaa 480
atgggagcca tccactgaga aaatgtatgc gcgtgatgga gtgctgaagg gtgatgttaa 540
catggctctg ttgcttgaag gaggtggcca ttaccgatgt gacttcaaaa ctacttacag 600
agctaagaag gttgtccagt tgccagacta tcattttgtg gaccatcgca ttgagattgt 660
gagccacgac aaagattaca acaagggttaa gctgtatgag catgccgaag ctcattctgg 720
gctgccgagg caggccaagt aaaggcttaa tgaaaagcca agacgacaac aaggagaaac 780
aaagtatttt ttttggttaa tttcaaggca tttactcgga attagtattt gatactttcg 840
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<210> 26

<211> 234

<212> PRT

<213> Montastraea cavernosa

<400> 26

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Met	Lys	Leu	Arg	Met	Glu	Gly	Ala	Val	Asn	Gly	His	Lys	Phe	Val	Ile				
		20					25				30								
Glu	Gly	Asp	Gly	Lys	Gly	Lys	Pro	Phe	Asp	Gly	Thr	Gln	Thr	Met	Asp				
	35					40					45								
Leu	Thr	Val	Ile	Glu	Gly	Ala	Pro	Leu	Pro	Phe	Ala	Tyr	Ala	Ile	Leu				
	50				55					60									
Thr	Thr	Val	Phe	Asp	Tyr	Gly	Asn	Arg	Val	Phe	Ala	Lys	Tyr	Pro	Glu				
65				70					75				80						
Asp	Ile	Ala	Asp	Tyr	Phe	Lys	Gln	Thr	Phe	Pro	Glu	Gly	Tyr	Phe	Trp				

				85					90					95			
Glu	Arg	Ser	Met	Thr	Tyr	Glu	Asp	Gln	Gly	Ile	Cys	Ile	Ala	Thr	Asn		
			100					105					110				
Asp	Ile	Thr	Met	Met	Lys	Gly	Val	Asp	Asp	Cys	Phe	Val	Tyr	Lys	Ile		
		115					120					125					
Arg	Phe	Asp	Gly	Val	Asn	Phe	Pro	Ala	Asn	Gly	Pro	Val	Met	Gln	Arg		
	130					135					140						
Lys	Thr	Leu	Lys	Trp	Glu	Pro	Ser	Thr	Glu	Lys	Met	Tyr	Ala	Arg	Asp		
	145				150					155					160		
Gly	Val	Leu	Lys	Gly	Asp	Val	Asn	Met	Ala	Leu	Leu	Leu	Glu	Gly	Gly		
			165					170						175			
Gly	His	Tyr	Arg	Cys	Asp	Phe	Lys	Thr	Thr	Tyr	Arg	Ala	Lys	Lys	Val		
		180						185					190				
Val	Gln	Leu	Pro	Asp	Tyr	His	Phe	Val	Asp	His	Arg	Ile	Glu	Ile	Val		
	195					200						205					
Ser	His	Asp	Lys	Asp	Tyr	Asn	Lys	Val	Lys	Leu	Tyr	Glu	His	Ala	Glu		
	210					215					220						
Ala	His	Ser	Gly	Leu	Pro	Arg	Gln	Ala	Lys								
225					230												

<210> 27
 <211> 1133
 <212> DNA
 <213> Montastraea annularis

<400> 27
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 agagcagatc gagaacacca agagctgtat tacgctaaaa tcttacttgc ctctaccacc 180
 atgagtatga ttaaaccaga aatgaagatc aagatgcgta tggacgggtgc tgtaaaccggg 240
 cacaagttcg tgattacagg ggaaggaagc ggcgagcctt tcgagggaaa acagactatg 300
 aacctgacag tcatagacgg cggacctctg ctttctgctt tcgacatctt gacaacagca 360
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 gatgggtgga actttcctgc caatagtcca gttatgcaga agaagaccgt gaaatgggag 600
 ccatgcactg rggaaatgta tgtgcgtgat ggagtgccta aagggtgtct taacatggct 660
 ctgttgcttg aaggaggtgg ccatttccga tgtgacttga aaactactta caaagctaag 720
 aagggtgtcc agatgccaga ctatcacttt gtgaatcacc gacttgagat aacatggcat 780
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 aggcaggcca aataaaggct tgacgaaaag ccaaaacggc aaagagtaca agaaagtata 900
 tataaatgta tatttttcaa ctgaaaggca ttccactcgg aattagttat tgatactttc 960
 aattcaagga tttatttttg gatttgctag ccactagctt tattgttaaa ttaagttaaa 1020
 gacggtttag cattttttcg gtattacaac ataggcacag acgtcttaac cccagtagtg 1080
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<210> 28
 <211> 224
 <212> PRT
 <213> Montastraea annularis

<220>
 <221> VARIANT
 <222> 65, 144
 <223> Xaa = Any Amino Acid

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		35					40					45					
Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Thr	Thr	Ala	Phe	Asp	Tyr	Gly		
	50					55					60						
Xaa	Arg	Val	Phe	Ala	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Phe	Lys		
65					70					75					80		
Gln	Ser	Phe	Pro	Glu	Gly	Phe	Ser	Trp	Glu	Arg	Ser	Met	Thr	Tyr	Glu		
			85						90					95			
Asp	Gly	Gly	Ile	Cys	Ile	Ala	Thr	Asn	Asp	Ile	Lys	Met	Glu	Gly	Asp		
		100					105						110				
Cys	Phe	Ser	Tyr	Glu	Ile	Arg	Phe	Asp	Gly	Val	Asn	Phe	Pro	Ala	Asn		
	115						120					125					
Ser	Pro	Val	Met	Gln	Lys	Lys	Thr	Val	Lys	Trp	Glu	Pro	Cys	Thr	Xaa		
	130					135					140						
Glu	Met	Tyr	Val	Arg	Asp	Gly	Val	Leu	Lys	Gly	Gly	Leu	Asn	Met	Ala		
145					150					155					160		
Leu	Leu	Leu	Glu	Gly	Gly	Gly	His	Phe	Arg	Cys	Asp	Leu	Lys	Thr	Thr		
			165						170					175			
Tyr	Lys	Ala	Lys	Lys	Val	Val	Gln	Met	Pro	Asp	Tyr	His	Phe	Val	Asn		
		180						185					190				
His	Arg	Leu	Glu	Ile	Thr	Trp	His	Asp	Glu	Asp	Tyr	Asn	Asn	Val	Lys		
	195						200					205					
Leu	Ser	Glu	His	Ala	Glu	Ala	His	Ser	Gly	Leu	Pro	Arg	Gln	Ala	Lys		
	210					215					220						